

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Behan, Dominic P.
5 Lehmann-Bruinsma, Karin
Chalmers, Derek T.
Lowitz, Kevin P.
Lin, I-Lin
Dang, Huong T.
10 Chen, Ruoping
Liaw, Chen W.
Gore, Martin J.
White, Carol

(ii) TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human
G Protein-Coupled Receptors

15 (iii) NUMBER OF SEQUENCES: 146

(iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Arena Pharmaceuticals, Inc.
(B) STREET: 6166 Nancy Ridge Drive
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92121

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (858)453-7200
(B) TELEFAX: (858)453-7210

(2) INFORMATION FOR SEQ ID NO:1:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATGGTCTTCT CGGCAGTGT GACTGCGTTC CATAACGGGA CATCCAACAC AACATTGTC	60
5	GTGTATGAAA ACACCTACAT GAATATTACA CTCCCTCCAC CATTCCAGCA TCCTGACCTC	120
	AGTCCATTGC TTAGATATAG TTTTGAAACC ATGGCTCCA CTGGTTGAG TTCCTTGACC	180
	GTGAATAGTA CAGCTGTGCC CACAACACCA GCAGCATTAGAGCCTAAA CTTGCCTCTT	240
	CAGATCACCC TTTCTGCTAT AATGATATTCA TTCTGTTG TGTCTTTCT TGGGAACCTG	300
	GTTGTTGCC TCATGGTTA CAAAAAGCT GCCATGAGGT CTGCAATTAA CATCCTCCTT	360
10	GCCAGCCTAG CTTTGCGAGA CATGTTGCTT GCAGTGCTGA ACATGCCCTT TGCCCTGGTA	420
	ACTATTCTTA CTACCCGATG GATTTTGAG AAATTCTTCT GTAGGGTATC TGCTATGTTT	480
	TTCTGGTTAT TTGTGATAGA AGGAGTAGCC ATCCTGCTCA TCATTAGCAT AGATAGGTTC	540
	CTTATTATAG TCCAGAGGCA GGATAAGCTA AACCCATATA GAGCTAAGGT TCTGATTGCA	600
	GTTTCTTGGG CAACTTCCTT TTGTGTTAGCT TTTCTTTAG CCGTAGGAAA CCCCACCTG	660
15	CAGATACCTT CCCGAGCTCC CCAGTGTGTG TTTGGGTACA CAACCAATCC AGGCTACCAG	720
	GCTTATGTGA TTTGATTTC TCTCATTCT TTCTTCATAC CCTTCCTGGT AATACTGTAC	780
	TCATTTATGG GCATACTCAA CACCCTCGG CACAATGCCT TGAGGATCCA TAGCTACCT	840
	GAAGGTATAT GCCTCAGCCA GGCCAGCAAA CTGGGTCTCA TGAGTCTGCA GAGACCTTC	900
	CAGATGAGCA TTGACATGGG CTTTAAAACA CGTGCCTTCA CCACTATTTT GATTCTTTT	960
20	GCTGTCTTCA TTGTCTGCTG GGCCCCATTCA ACCACTTACA GCCTTGTGGC AACATTCACT	1020
	AAGCACTTTT ACTATCAGCA CAACTTTTT GAGATTAGCA CCTGGCTACT GTGGCTCTGC	1080
	TACCTCAAGT CTGCATTGAA TCCGCTGATC TACTACTGGA GGATTAAGAA ATTCCATGAT	1140
	GCTTGCCTGG ACATGATGCC TAAGTCCTTC AAGTTTTGC CGCAGCTCCC TGGTCACACA	1200
	AAGCGACGGA TACGTCCCTAG TGCTGTCTAT GTGTGTGGGG AACATCGGAC GGTGGTGTGA	1260

25 (3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS.

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn
1 5 10 15

5 Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro
20 25 30

Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
35 40 45

Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
10 50 55 60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
65 70 75 80

Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
85 90 95

15 Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met
100 105 110

Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met
115 120 125

Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr
20 130 135 140

Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe
145 150 155 160

Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser
165 170 175

25 Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro
180 185 190

Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys
195 200 205

30 Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser
210 215 220

Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln
225 230 235 240

Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu
245 250 255

35 Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn
260 265 270

	Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala			
	275	280	285	
	Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile			
	290	295	300	
5	Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe			
	305	310	315	320
	Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val			
	325	330	335	
10	Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile			
	340	345	350	
	Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro			
	355	360	365	
	Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp			
	370	375	380	
15	Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr			
	385	390	395	400
	Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg			
	405	410	415	
	Thr Val Val			
20				

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	ATGTTAGCCA ACAGCTCCTC AACCAACAGT TCTGTTCTCC CGTGTCCCTGA CTACCGACCT	60
30	ACCCACCGCC TGCACTTGGT GGTCTACAGC TTGGTGCTGG CTGCCGGGCT CCCCCCTCAAC	120
	GCGCTAGCCC TCTGGGTCTT CCTGCGCGCG CTGCGCGTGC ACTCGGTGGT GAGCGTGTAC	180
	ATGTGTAACC TGGCGGCCAG CGACCTGCTC TTCAACCCTCT CGCTGCCCGT TCGTCTCTCC	240
	TACTACGCAC TGCACCACTG GCCCTTCCCC GACCTCCTGT GCCAGACGAC GGGCGCCATC	300
	TTCCAGATGA ACATGTACGG CAGCTGCATC TTCCCTGATGC TCATCAACGT GGACCGCTAC	360

	GCCGCCATCG	TGCACCCGCT	GCGACTGCGC	CACCTGCGGC	GGCCCCGCGT	GGCGCGGCTG	420
	CTCTGCCTGG	GCGTGTGGC	GTCATCCTG	GTGTTGCCG	TGCCCGCCGC	CCGCGTGCAC	480
	AGGCCCTCGC	GTTGCCGCTA	CGGGGACCTC	GAGGTGCGCC	TATGCTTCGA	GAGCTTCAGC	540
	GACGAGCTGT	GGAAAGGCAG	GCTGCTGCC	CTCGTGCTGC	TGGCCGAGGC	GCTGGGCTTC	600
5	CTGCTGCC	TGGCGCGGT	GGTCTACTCG	TCGGGCCGAG	TCTTCTGGAC	GCTGGCGCGC	660
	CCCGACGCCA	CGCAGAGCCA	GCGGCCGG	AAGACCGTGC	GCCTCCTGCT	GGCTAACCTC	720
	GTCATCTTCC	TGCTGTGCTT	CGTGCCCTAC	AACAGCACGC	TGGCGGTCTA	CGGGCTGCTG	780
	CGGAGCAAGC	TGGTGGCGGC	CAGCGTGCCT	GCCCGCGATC	GCGTGCAGCG	GGTGCCTGATG	840
	GTGATGGTGC	TGCTGGCCGG	CGCCAACACTGC	GTGCTGGACC	CGCTGGTGTA	CTACTTTAGC	900
10	GCCGAGGGCT	TCCGCAACAC	CCTGCGCGGC	CTGGGCACTC	CGCACCGGGC	CAGGACCTCG	960
	GCCACCAACG	GGACGCGGGC	GGCGCTCGCG	CAATCCGAAA	GGTCCGCCGT	CACCACCGAC	1020
	GCCACCAGGC	CGGATGCCGC	CAGTCAGGGG	CTGCTCCGAC	CCTCCGACTC	CCACTCTCTG	1080
	TCTTCCTTCA	CACAGTGTCC	CCAGGATTCC	GCCCTCTGA			1119

(5) INFORMATION FOR SEQ ID NO:4:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Leu	Ala	Asn	Ser	Ser	Ser	Thr	Asn	Ser	Ser	Val	Leu	Pro	Cys	Pro
	1				5					10					15	
25	Asp	Tyr	Arg	Pro	Thr	His	Arg	Leu	His	Leu	Val	Val	Tyr	Ser	Leu	Val
				20					25				30			
	Leu	Ala	Ala	Gly	Leu	Pro	Leu	Asn	Ala	Leu	Ala	Leu	Trp	Val	Phe	Leu
				35				40				45				
	Arg	Ala	Leu	Arg	Val	His	Ser	Val	Val	Ser	Val	Tyr	Met	Cys	Asn	Leu
				50			55				60					
30	Ala	Ala	Ser	Asp	Leu	Leu	Phe	Thr	Leu	Ser	Leu	Pro	Val	Arg	Leu	Ser
				65			70			75			80			
	Tyr	Tyr	Ala	Leu	His	His	Trp	Pro	Phe	Pro	Asp	Leu	Leu	Cys	Gln	Thr

	85	90	95
	Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu		
	100	105	110
5	Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg		
	115	120	125
	Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly		
	130	135	140
	Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His		
	145	150	155
10	Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe		
	165	170	175
	Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val		
	180	185	190
15	Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val		
	195	200	205
	Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr		
	210	215	220
	Gln Ser Gln Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu		
	225	230	235
20	Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val		
	245	250	255
	Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg		
	260	265	270
25	Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala		
	275	280	285
	Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe		
	290	295	300
	Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser		
	305	310	315
30	Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala		
	325	330	335
	Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu		
	340	345	350
	Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln		
35	355	360	365
	Asp Ser Ala Leu		
	370		

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCCA	ACT CCACAGGGCT	GAACGCC	TC	GAAGTCG	CAG G	GCTCGT	GGG GTT	GATC	CCTG	60	
10 GCAGCTG	TCG TGGAGGT	GGG GGC	ACTG	CTG GGCA	ACCGG	CGCTG	CTGGT	CGTGG	TGCTG	120	
CGCACGCC	GG GACTGCG	CGCG	CTCTAC	CTGGCG	CACC TGTG	TGTGCG	CGT	GGAC	CTGCTG	180	
GC	GGCCGC	CC	CATCATGCC	GCTGGC	CTGGCG	CAC	CGCCG	CCC	GG GCTGGCC	240	
TGCGC	CTGG	GCCCGCG	ATGCCG	GCGCC	GCTCG	CTTCC	TCTCC	GCCG	TCTGCTGCC	300	
GCCTG	CACGC	TCGGGT	GGC CGC	ACTTGGC	CTGGCAC	GCT ACC	GGC	CCTCAT	CGTGCACCCG	360	
15 CTGCGGCC	AG GCTCG	CGG	CCTGTG	CTCGT	GCTCA	CCGCG	TGTG	GGCG	CGCGCG	420	
GGACTG	CTGG	GCG	GCTCTC	CCTG	CGCG	CCGCC	CCCG	CACCG	CCCC	480	
CGCTG	CTCGG	TCCTGG	GGGC	CTCGG	CCCTTCC	CGCT	CTGGG	CCTG	GCTGCC	540	
TTCG	CGCTG	CCGCC	CTC	GCTCG	GCCTAC	GGCG	GCAT	TTCGT	GGTGGCG	600	
CGCG	CTGCC	TGAGG	CCCC	ACGGCC	GGCG	CGCGGG	TCCC	GACTCC	GCTC	660	
20 GATAGCC	GGCC	TTTCC	CATCTT	GCCG	CCGCT	CGG	CTCGCC	TGCCC	GGGG	CAAGGCG	720
CTGG	CCCC	AG	CGCTGG	CCGT	GGCCA	ATT	TGAGC	CTG	GGCTG	CGCG	780
TGC	CTGG	CGC	CAGCG	CG	GGCG	GGAA	GCGAAG	CGG	CTGTC	ACCTG	840
TCGG	CCTTC	CGG	CTCAC	CCC	CTTCC	GTAC	GGG	CTGCT	GC	TGCAAG	900
CTGG	CCGCC	TCT	CTCG	CCC	TGC	ACTGC	GGAC	CTGTG	GC	GGCTTG	960
25 TGGCAC	CCCGC	GGG	CACTCTT	GCAAT	GCCTC	CAGA	GACCCC	CAGAGG	GGCCC	TGCCGTAG	1020
CCTT	CTGAGG	CTCC	AAGAAC	GAC	CCC	GGAG	TTGGC	AGGAG	GGCG	GAGCCC	1080
GGGC	CACCTG	AGAG	TTCTCT	CTC	CTG	AGT	CTCT	CTCT	CGC	ATACCAG	1107

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 368 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala Gly Ser Leu
1 5 10 15

Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn
20 25 30

10 Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
35 40 45

Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser
50 55 60

15 Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
65 70 75 80

Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
85 90 95

Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
100 105 110

20 Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
115 120 125

Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly
130 135 140

25 Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
145 150 155 160

Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
165 170 175

Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Gly Ala Tyr
180 185 190

30 Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg
195 200 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu
210 215 220

35 Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala
225 230 235 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro

	245	250	255
	Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu		
	260	265	270
5	Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe		
	275	280	285
	Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu		
	290	295	300
	Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala		
	305	310	315
10	Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly		
	325	330	335
	Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala		
	340	345	350
15	Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser		
	355	360	365

(8) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1008 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	ATGGAATCAT CTTTCTCATT TGGAGTGATC CTTGCTGTCC TGGCCTCCCT CATCATTGCT	60
25	ACTAACACAC TAGTGGCTGT GGCTGTGCTG CTGTTGATCC ACAAGAATGA TGGTGTCACT	120
	CTCTGCTTCA CCTTGAATCT GGCTGTGGCT GACACCTTGA TTGGTGTGGC CATCTCTGGC	180
	CTACTCACAG ACCAGCTCTC CAGCCCTTCT CGGCCACAC AGAAGACCCT GTGCAGCCTG	240
	CGGATGGCAT TTGTCACTTC CTCCGCAGCT GCCTCTGTCC TCACGGTCAT GCTGATCACC	300
	TTTGACAGGT ACCTTGCCAT CAAGCAGCCC TTCCGCTACT TGAAGATCAT GAGTGGGTT	360
30	GTGGCCGGGG CCTGCATTGC CGGGCTGTGG TTAGTGTCTT ACCTCATTGG CTTCCCTCCCA	420
	CTCGGAATCC CCATGTTCCA GCAGACTGCC TACAAAGGGC AGTGCAGCTT CTTTGCTGTA	480
	TTTCACCCCTC ACTTCGTGCT GACCCTCTCC TGCCTGGCT TCTTCCCAGC CATGCTCCTC	540
	TTTGTCTTCT TCTACTGCGA CATGCTCAAG ATTGCCTCCA TGCACAGCCA GCAGATTGCA	600

AAGATGGAAC ATGCAGGAGC CATGGCTGGA GGTTATCGAT CCCCACGGAC TCCCAGCGAC	660
TTCAAAGCTC TCCGTACTGT GTCTGTTCTC ATTGGGAGCT TTGCTCTATC CTGGACCCCC	720
TTCCTTATCA CTGGCATTGT GCAGGTGGCC TGCCAGGAGT GTCACCTCTA CCTAGTGCTG	780
GAACGGTACC TGTGGCTGCT CGGCGTGGC AACTCCCTGC TCAACCCACT CATCTATGCC	840
5 TATTGGCAGA AGGAGGTGCG ACTGCAGCTC TACCACATGG CCCTAGGAGT GAAGAAGGTG	900
CTCACCTCAT TCCTCCTCTT TCTCTCGGCC AGGAATTGTG GCCCAGAGAG GCCCAGGGAA	960
AGTTCCCTGTC ACATCGTCAC TATCTCCAGC TCAGAGTTTG ATGGCTAA	1008

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser			
1	5	10	15
Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu			
20	25	30	
20 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala			
35	40	45	
Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp			
50	55	60	
25 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu			
65	70	75	80
Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val			
85	90	95	
Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg			
100	105	110	
30 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly			
115	120	125	
Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro			
130	135	140	
Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val			

	145	150	155	160
	Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro			
	165	170	175	
5	Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala			
	180	185	190	
	Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met			
	195	200	205	
	Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu			
	210	215	220	
10	Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro			
	225	230	235	240
	Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu			
	245	250	255	
15	Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser			
	260	265	270	
	Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu			
	275	280	285	
	Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe			
	290	295	300	
20	Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu			
	305	310	315	320
	Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly			
	325	330	335	

(10) INFORMATION FOR SEQ ID NO:9:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGACACTA CCATGGAAGC TGACCTGGGT GCCACTGGCC ACAGGGCCCG CACAGAGCTT	60
GATGATGAGG ACTCCTACCC CCAAGGTGGC TGGGACACGG TCTTCCTGGT GGCCCTGCTG	120
CTCCTTGGGC TGCCAGCCAA TGGGTTGATG GCGTGGCTGG CCGGCTCCCA GGCCCGGCAT	180
35 GGAGCTGGCA CGCGTCTGGC GCTGCTCCTG CTCAGCCTGG CCCTCTCTGA CTTCTTGTTC	240

CTGGCAGCAG CGGCCTTCCA GATCCTAGAG ATCCGGCATG GGGGACACTG GCCGCTGGGG 300
 ACAGCTGCCT GCCGCTTCTA CTACTTCCTA TGGGGCGTGT CCTACTCCTC CGGCCTCTTC 360
 CTGCTGGCCG CCCTCAGCCT CGACCGCTGC CTGCTGGCGC TGTGCCACA CTGGTACCCCT 420
 GGGCACCGCC CAGTCCGCCT GCCCCCTCTGG GTCTGCGCCG GTGCTGGGT GCTGGCCACA 480
 5 CTCTTCAGCG TGCCCTGGCT GGTCTTCCCC GAGGCTGCG TCTGGTGGTA CGACCTGGTC 540
 ATCTGCCTGG ACTTCTGGGA CAGCGAGGAG CTGTCGCTGA GGATGCTGGA GGTCCTGGGG 600
 GGCTTCCTGC CTTTCCTCCT GCTGCTCGTC TGCCACGTGC TCACCCAGGC CACAGCCTGT 660
 CGCACCTGCC ACCGCCAACA GCAGCCCGCA GCCTGCCGGG GCTTCGCCCCG TGTGGCCAGG 720
 ACCATTCTGT CAGCCTATGT GGTCCTGAGG CTGCCCTACC AGCTGGCCA GCTGCTCTAC 780
 10 CTGGCCTTCC TGTGGGACGT CTACTCTGGC TACCTGCTCT GGGAGGCCCT GGTCTACTCC 840
 GACTACCTGA TCCTACTCAA CAGCTGCCTC AGCCCCTTCC TCTGCCTCAT GGCCAGTGCC 900
 GACCTCCGGA CCCTGCTGCG CTCCGTGCTC TCGTCCTTCG CGGCAGCTCT CTGCGAGGAG 960
 CGGCCGGGCA GCTTCACGCC CACTGAGCCA CAGACCCAGC TAGATTCTGA GGGTCCAACCT 1020
 CTGCCAGAGC CGATGGCAGA GGCCCAGTCA CAGATGGATC CTGTGGCCA GCCTCAGGTG 1080
 15 AACCCCACAC TCCAGCCACG ATCGGATCCC ACAGCTCAGC CACAGCTGAA CCCTACGGCC 1140
 CAGCCACAGT CGGATCCCAC AGCCCAGCCA CAGCTGAACC TCATGGCCA GCCACAGTCA 1200
 GATTCTGTGG CCCAGGCCACA GGCAAGACACT AACGTCCAGA CCCCTGCACC TGCTGCCAGT 1260
 TCTGTGCCCA GTCCCTGTGA TGAAGCTTCC CCAACCCAT CCTCGCATCC TACCCAGGG 1320
 GCCCTTGAGG ACCCAGGCCAC ACCTCCTGCC TCTGAAGGAG AAAGCCCCAG CAGCACCCCG 1380
 20 CCAGAGGGCGG CCCCGGGCGC AGGCCCCACG TGA 1413

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro

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Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp
20 25 30

Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly
35 40 45

5 Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr
50 55 60

Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe
65 70 75 80

Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His
10 85 90 95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly
100 105 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp
115 120 125

15 Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro
130 135 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr
145 150 155 160

20 Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp
165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser
180 185 190

Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu
195 200 205

25 Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln
210 215 220

Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile
225 230 235 240

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu
30 245 250 255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp
260 265 270

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu
275 280 285

35 Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu
290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Leu Cys Glu Glu Arg Pro

	305	310	315	320
	Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly			
	325	330	335	
5	Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro			
	340	345	350	
	Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro			
	355	360	365	
	Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro			
	370	375	380	
10	Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser			
	385	390	395	400
	Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala			
	405	410	415	
15	Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser			
	420	425	430	
	Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala			
	435	440	445	
	Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly			
	450	455	460	
20	Ala Gly Pro Thr			
	465			

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30	ATGTCAGGGA TGGAAAAACT TCAGAATGCT TCCTGGATCT ACCAGCAGAA ACTAGAAGAT	60
	CCATTCCAGA AACACCTGAA CAGCACCGAG GAGTATCTGG CCTTCCTCTG CGGACCTCGG	120
	CGCAGCCACT TCTTCCTCCC CGTGTCTGTG GTGTATGTGC CAATTTTGTT GGTGGGGGTC	180
	ATTGGCAATG TCCTGGTGTG CCTGGTGATT CTGCAGCACC AGGCTATGAA GACGCCACC	240
	AACTACTACC TCTTCAGCCT GGCGGTCTCT GACCTCCTGG TCCTGCTCCT TGGAATGCC	300

CTGGAGGTCT	ATGAGATGTG	GCGCAACTAC	CCTTCCTTGT	TCGGGCCCGT	GGGCTGCTAC	360	
TTCAAGACGG	CCCTCTTGA	GACCGTGTGC	TCGCCTCCA	TCCTCAGCAT	CACCACCGTC	420	
AGCGTGGAGC	GCTACGTGGC	CATCCTACAC	CCGTTCCGCG	CCAAACTGCA	GAGCACCCGG	480	
CGCCGGGCC	TCAGGATCCT	CGGCATCGTC	TGGGGCTTCT	CCGTGCTCTT	CTCCCTGCC	540	
5	AACACCAGCA	TCCATGGCAT	CAAGTTCCAC	TACTTCCCCA	ATGGGTCCT	GGTCCCAGGT	600
	TCGGCCACCT	GTACGGTCAT	CAAGCCCAG	TGGATCTACA	ATTCATCAT	CCAGGTCACC	660
	TCCTTCCTAT	TCTACCTCCT	CCCCATGACT	GTCATCAGTG	TCCTCTACTA	CCTCATGGCA	720
	CTCAGACTAA	AGAAAGACAA	ATCTCTTGAG	GCAGATGAAG	GGAATGCAA	TATTCAAAGA	780
	CCCTGCAGAA	AATCAGTCAA	CAAGATGCTG	TTTGTCTTGG	TCTTAGTGTT	TGCTATCTGT	840
10	TGGGGCCCGT	TCCACATTGA	CCGACTCTTC	TTCAGCTTG	TGGAGGAGTG	GAGTGAATCC	900
	CTGGCTGCTG	TGTTCAACCT	CGTCCATGTG	GTGTCAGGTG	TCTTCTTCTA	CCTGAGCTCA	960
	GCTGTCAACC	CCATTATCTA	TAACCTACTG	TCTGCCGCT	TCCAGGCAGC	ATTCCAGAAT	1020
	GTGATCTCTT	CTTTCCACAA	ACAGTGGCAC	TCCCAGCATG	ACCCACAGTT	GCCACCTGCC	1080
	CAGCGGAACA	TCTTCCTGAC	AGAATGCCAC	TTTGTGGAGC	TGACCGAAGA	TATAGGTCCC	1140
15	CAATTCCCAT	GTCAGTCATC	CATGCACAAAC	TCTCACCTCC	CAACAGCCCT	CTCTAGTGAA	1200
	CAGATGTCAA	GAACAAACTA	TCAAAGCTTC	CACTTTAACAA	AAACCTGA		1248

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25	Met	Ser	Gly	Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln
	1			5				10				15				
	Lys	Leu	Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr
	20			25				30								
30	Leu	Ala	Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val
	35			40				45								
	Ser	Val	Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val

	50	55	60
	Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr		
	65	70	75
	Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu		
5	85	90	95
	Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe		
	100	105	110
	Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr		
	115	120	125
10	Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg		
	130	135	140
	Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg		
	145	150	155
	Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu		
15	165	170	175
	Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe		
	180	185	190
	Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys		
	195	200	205
20	Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe		
	210	215	220
	Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala		
	225	230	235
	Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala		
25	245	250	255
	Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val		
	260	265	270
	Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg		
	275	280	285
30	Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val		
	290	295	300
	Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser		
	305	310	315
	Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala		
35	325	330	335
	Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln		
	340	345	350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
 355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
 370 375 380

5 Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
 385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
 405 410 415

(14) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCAGATA CTAATAGCAC AATCAATTAA TCACTAAGCA CTCGTGTTAC TTTAGCATT	60
TTTATGTCCT TAGTAGCTTT TGCTATAATG CTAGGAAATG CTTTGGTCAT TTTAGCTTT	120
GTGGTGGACA AAAACCTTAG ACATCGAAGT AGTTATTTTT TTCTTAACCTT GGCCATCTCT	180
20 GACTTCTTG TGGGTGTGAT CTCCATTCTT TTGTACATCC CTCACACGCT GTTCGAATGG	240
GATTTGGAA AGGAAATCTG TGTATTTGG CTCACTACTG ACTATCTGTT ATGTACAGCA	300
TCTGTATATA ACATTGTCCT CATCAGCTAT GATCGATACC TGTCAGTCTC AAATGCTGTG	360
TCTTATAGAA CTCAACATAC TGGGGTCTTG AAGATTGTTA CTCTGATGGT GGCGTTGG	420
GTGCTGGCCT TCTTAGTGAA TGGGCCAATG ATTCTAGTTT CAGAGTCTTG GAAGGATGAA	480
25 GGTAGTGAAT GTGAACCTGG ATTTTTTCG GAATGGTACA TCCTTGCCAT CACATCATT	540
TTGGAATTCTG TGATCCCAGT CATCTTAGTC GCTTATTCA ACATGAATAT TTATTGGAGC	600
CTGTGGAAGC GTGATCATCT CAGTAGGTGC CAAAGCCATC CTGGACTGAC TGCTGTCTCT	660
TCCAACATCT GTGGACACTC ATTCAAGAGGT AGACTATCTT CAAGGAGATC TCTTCTGCA	720
TCGACAGAAG TTCCTGCATC CTTTCATTCA GAGAGACAGA GGAGAAAGAG TAGTCTCATG	780
30 TTTCCCTCAA GAACCAAGAT GAATAGCAAT ACAATTGCTT CCAAAATGGG TTCCCTCTCC	840
CAATCAGATT CTGTAGCTCT TCACCAAAGG GAACATGTTG AACTGCTTAG AGCCAGGAGA	900

TTAGCCAAGT CACTGGCCAT TCTCTTAGGG GTTTTGCTG TTTGCTGGC TCCATATTCT 960
 CTGTTCACAA TTGTCCTTTC ATTTTATTCC TCAGCAACAG GTCCTAAATC AGTTTGGTAT 1020
 AGAATTGCAT TTTGGCTTCA GTGGTTCAAT TCCTTGTCATCCTCTTT GTATCCATTG 1080
 TGTCACAAGC GCTTTCAAAA GGCTTCTTG AAAATATTTT GTATAAAAAAA GCAACCTCTA 1140
 5 CCATCACAAAC ACAGTCGGTC AGTATCTTCT TAA 1173

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 390 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

15 Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val
 1 5 10 15

Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly
 20 25 30

Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
 35 40 45

20 Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
 50 55 60

Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
 65 70 75 80

Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
 25 85 90 95

Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg
 100 105 110

Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly
 115 120 125

30 Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe
 130 135 140

Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu
 145 150 155 160

Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala
 35 165 170 175

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr
 180 185 190
 Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser
 195 200 205
 5 Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys
 210 215 220
 Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala
 225 230 235 240
 Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys
 10 245 250 255
 Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile
 260 265 270
 Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His
 275 280 285
 15 Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser
 290 295 300
 Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser
 305 310 315 320
 Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys
 20 325 330 335
 Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe
 340 345 350
 Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala
 355 360 365
 25 Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His
 370 375 380
 Ser Arg Ser Val Ser Ser
 385 390

(16) INFORMATION FOR SEQ ID NO:15:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAAGCTTA ACGATCCCCA GGAGCAACAT

30

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGGGATCCT ACGAGAGCAT TTTTCACACA G
31

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCGAACG	CGAGCGAGCC	GGGTGGCAGC	GGCGGCGGCG	AGGCGGCCGC	CCTGGCCTC	60
AAGCTGGCCA	CGCTCAGCCT	GCTGCTGTGC	GTGAGCCTAG	CGGGCAACGT	GCTGTTCGCG	120
CTGCTGATCG	TGCGGGAGCG	CAGCCTGCAC	CGCGCCCCGT	ACTACCTGCT	GCTCGACCTG	180
TGCCTGGCCG	ACGGGCTGCG	CGCGCTCGCC	TGCCTCCCGG	CCGTCATGCT	GGCGGCGCGG	240
25 CGTGCGGCGG	CCGCGGCGGG	GGCGCCGCCG	GGCGCGCTGG	GCTGCAAGCT	GCTCGCCTTC	300
CTGGCCGCGC	TCTTCTGCTT	CCACGCCGCC	TTCCTGCTGC	TGGGCGTGGG	CGTCACCCGC	360
TACCTGGCCA	TCGCGCACCA	CCGCTCTAT	GCAGAGCGCC	TGGCCGGCTG	GCCGTGCGCC	420
GCCATGCTGG	TGTGCGCCGC	CTGGGCGCTG	GCGCTGGCCG	CGGCCTTCCC	GCCAGTGCTG	480
GACGGCGGTG	GCGACGACGA	GGACGCGCCG	TGCGCCCTGG	AGCAGCGGCC	CGACGGCGCC	540
30 CCCGGCGCGC	TGGGCTTCCT	GCTGCTGCTG	GCCGTGGTGG	TGGGCGCCAC	GCACCTCGTC	600
TACCTCCGCC	TGCTCTTCTT	CATCCACGAC	CGCCGCAAGA	TGCGGCCCGC	GCGCCTGGTG	660

CCCGCCGTCA GCCACGACTG GACCTTCCAC GGCCCCGGCG CCACCGGCCA GGCGGCCGCC 720
 AACTGGACGG CGGGCTTCGG CCGCGGGCCC ACGCCGCCCG CGCTTGTGGG CATCCGGCCC 780
 GCAGGGCCGG GCCCGGGCGC GCGCCGCCTC CTCGTGCTGG AAGAATTCAA GACGGAGAAG 840
 AGGCTGTGCA AGATGTTCTA CGCCGTCACG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC 900
 5 GTCGTGGCCA GCTACCTGCG GGTCCCTGGTG CGGCCCGGGCG CCGTCCCCCA GGCCTACCTG 960
 ACGGCCTCCG TGTGGCTGAC CTTCGCCAG GCCGGCATCA ACCCCGTCGT GTGCTTCCTC 1020
 TTCAACAGGG AGCTGAGGGGA CTGCTTCAGG GCCCAGTTCC CCTGCTGCCA GAGCCCCCGG 1080
 ACCACCCAGG CGACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA 1128

(19) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
 1 5 10 15
 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
 20 25 30
 Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
 35 40 45
 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
 50 55 60
 25 Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
 65 70 75 80
 Arg Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
 85 90 95
 Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
 30 100 105 110
 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
 115 120 125
 Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
 130 135 140

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PATENT

Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Phe Pro Pro Val Leu
145 150 155 160

Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
165 170 175

5 Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Ala Val
180 185 190

Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
195 200 205

10 His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
210 215 220

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala
225 230 235 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
245 250 255

15 Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
260 265 270

Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
275 280 285

20 Val Thr Leu Leu Phe Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
290 295 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu
305 310 315 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val
325 330 335

25 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
340 345 350

Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
355 360 365

30 Asp Leu Lys Gly Ile Gly Leu
370 375

(20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGAACACCA CAGTGATGCA AGGCTTCAAC AGATCTGAGC GGTGCCAG AGACACTCGG 60
 ATAGTACAGC TGGTATTCCC AGCCCTCTAC ACAGTGGTTT TCTTGACCGG CATCCTGCTG 120
 AATACTTGG CTCTGTGGGT GTTTGTTCAC ATCCCCAGCT CCTCCACCTT CATCATCTAC 180
 5 CTCAAAAACA CTTGGTGGC CGACTTGATA ATGACACTCA TGCTTCCTT CAAAATCCTC 240
 TCTGACTCAC ACCTGGCACC CTGGCAGCTC AGAGCTTTG TGTGTCGTTT TTCTTCGGTG 300
 ATATTTATG AGACCATGTA TGTGGGCATC GTGCTGTTAG GGCTCATAGC CTTTGACAGA 360
 TTCCCTCAAGA TCATCAGACC TTTGAGAAAT ATTTTCTAA AAAAACCTGT TTTTGCAAAA 420
 ACGGTCTCAA TCTTCATCTG GTTCTTTTG TTCTTCATCT CCCTGCCAAA TACGATCTG 480
 10 AGCAACAAAG AAGCAACACC ATCGTCTGTG AAAAAGTGTG CTTCCCTAAA GGGGCCTCTG 540
 GGGCTGAAAT GGCATCAAAT GGTAAATAAC ATATGCCAGT TTATTTCTG GACTGTTTT 600
 ATCCTAATGC TTGTGTTTA TGTGGTTATT GCAAAAAAG TATATGATTG TTATAGAAAG 660
 TCCAAAAGTA AGGACAGAAA AAACAACAAA AAGCTGGAAG GCAAAGTATT TGTTGTCGTG 720
 GCTGTCTTCT TTGTGTGTT TGCTCCATT CATTGCCA GAGTTCCATA TACTCACAGT 780
 15 CAAACCAACA ATAAGACTGA CTGTAGACTG CAAATCAAC TGTTTATTGC TAAAGAAACA 840
 ACTCTCTTT TGGCAGCAAC TAACATTGT ATGGATCCCT TAATATACAT ATTCTTATGT 900
 AAAAATTCA CAGAAAAGCT ACCATGTATG CAAGGGAGAA AGACCACAGC ATCAAGCCAA 960
 GAAAATCATA GCAGTCAGAC AGACAAACATA ACCTTAGGCT GA 1002

(21) INFORMATION FOR SEQ ID NO:20:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Asn	Thr	Thr	Val	Met	Gln	Gly	Phe	Asn	Arg	Ser	Glu	Arg	Cys	Pro
1															15
Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val															
30															30
20 25															

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
 35 40 45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
 50 55 60

5 Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
 65 70 75 80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
 85 90 95

10 Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
 100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu
 115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile
 130 135 140

15 Phe Ile Trp Phe Phe Leu Phe Ile Ser Leu Pro Asn Thr Ile Leu
 145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu
 165 170 175

20 Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys
 180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val
 195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys
 210 215 220

25 Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val
 225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro
 245 250 255

30 Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
 260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
 275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
 290 295 300

35 Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
 305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly

325

330

(22) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10	ATGGCCAACA CTACCGGAGA GCCTGAGGAG GTGAGCGGCG CTCTGTCCCC ACCGTCCGCA	60
	TCAGCTTATG TGAAGCTGGT ACTGCTGGGA CTGATTATGT GCGTGAGCCT GGCGGGTAAC	120
	GCCATCTTGT CCCTGCTGGT GCTCAAGGAG CGTGCCTGTC ACAAGGCTCC TTACTACTTC	180
	CTGCTGGACC TGTGCCTGGC CGATGGCATA CGCTCTGCCG TCTGCTTCCC CTTTGTGCTG	240
	GCTTCTGTGC GCCACGGCTC TTCATGGACC TTCAGTGCAC TCAGCTGCAA GATTGTGGCC	300
15	TTTATGGCCG TGCTCTTTTG CTTCCATGCG GCCTTCATGC TGTTCTGCAT CAGCGTCACC	360
	CGCTACATGG CCATCGCCCA CCACCGCTTC TACGCCAAGC GCATGACACT CTGGACATGC	420
	GCGGCTGTCA TCTGCATGGC CTGGACCTG TCTGTGGCCA TGGCCTTCCC ACCTGTCTTT	480
	GACGTGGGCA CCTACAAGTT TATTGGGAG GAGGACCAAGT GCATCTTGA GCATCGCTAC	540
	TTCAAGGCCA ATGACACGCT GGGCTTCATG CTTATGTTGG CTGTGCTCAT GGCAGCTACC	600
20	CATGCTGTCT ACGGCAAGCT GCTCCTCTTC GAGTATCGTC ACCGCAAGAT GAAGCCAGTG	660
	CAGATGGTGC CAGCCATCAG CCAGAACTGG ACATTCCATG GTCCCGGGGC CACCGGCCAG	720
	GCTGCTGCCA ACTGGATCGC CGGCTTGGC CGTGGGCCA TGCCACCAAC CCTGCTGGGT	780
	ATCCGGCAGA ATGGGCATGC AGCCAGCCGG CGGCTACTGG GCATGGACGA GGTCAAGGGT	840
	GAAAAGCAGC TGGGCCGCAT GTTCTACGCG ATCACACTGC TCTTCTGCT CCTCTGGTCA	900
25	CCCTACATCG TGGCCTGCTA CTGGCGAGTG TTTGTGAAAG CCTGTGCTGT GCCCCACCGC	960
	TACCTGGCCA CTGCTGTTTG GATGAGCTTC GCCCAGGCTG CCGTCAACCC AATTGTCTGC	1020
	TTCCTGCTCA ACAAGGACCT CAAGAAGTGC CTGACCACTC ACGCCCCCTG CTGGGGCACA	1080
	GGAGGTGCCG CGGCTCCAG AGAACCTAC TGTGTCATGT GA	1122

(23) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
5 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1 5 10 15

10 Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
20 25 30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
35 40 45

15 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
50 55 60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
65 70 75 80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
85 90 95

20 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
100 105 110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
115 120 125

25 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
130 135 140

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
145 150 155 160

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
165 170 175

30 Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
195 200 205

35 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 5 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300
 10 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320
 Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335
 Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr
 340 345 350
 15 Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365
 Pro Tyr Cys Val Met
 370
 (24) INFORMATION FOR SEQ ID NO:23:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1053 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGGCTTG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC 60
 ACTTATGACT ACAGTCATA TGAATTGATC TGTATCAAAG AAGATGTCAG AGAATTTGCA 120
 AAAGTTTCC TCCCTGTATT CCTCACAATA GCTTTCGTCA TTGGACTTGC AGGCAATTCC 180
 30 ATGGTAGTGG CAATTTATGC CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC 240
 CTGAATTG 300 CTGTAGCAGA TTTACTCCTT CTATTCACTC TGCCTTTTG GGCTGTTAAT
 GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC CTTGTACACA 360
 CTAAACTTTG TCTCTGGAAT GCAGTTCTG GCTTGCATCA GCATAGACAG ATATGTGGCA 420
 GTAACTAATG TCCCCAGCCA ATCAGGAGTG GGAAAACCAG GCTGGATCAT CTGTTCTGT 480

GTCTGGATGG	CTGCCATCTT	GCTGAGCATA	CCCCAGCTGG	TTTTTTATAC	AGTAAATGAC	540	
AATGCTAGGT	GCATTCCCAT	TTTCCCCGC	TACCTAGGAA	CATCAATGAA	AGCATTGATT	600	
CAAATGCTAG	AGATCTGCAT	TGGATTGTA	GTACCCTTC	TTATTATGGG	GGTGTGCTAC	660	
TTTATCACGG	CAAGGACACT	CATGAAGATG	CCAAACATTA	AAATATCTG	ACCCCTAAAA	720	
5	GTTCTGCTCA	CAGTCGTTAT	AGTTTCATT	GTCACTCAAC	TGCCTTATAA	CATTGTCAAG	780
TTCTGCCGAG	CCATAGACAT	CATCTACTCC	CTGATCACCA	GCTGCAACAT	GAGCAAACGC	840	
ATGGACATCG	CCATCCAAGT	CACAGAAAGC	ATTGCACTCT	TTCACAGCTG	CCTCAACCCA	900	
ATCCTTTATG	TTTTTATGGG	AGCATCTTC	AAAAACTACG	TTATGAAAGT	GGCCAAGAAA	960	
TATGGGTCC	GGAGAAGACA	GAGACAAAGT	GTGGAGGAGT	TTCCTTTGA	TTCTGAGGGT	1020	
10	CCTACAGAGC	CAACCAAGTAC	TTTTAGCATT	TAA		1053	

(25) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

20	Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn					
	1	5	10	15		
	Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile					
	20	25	30			
	Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu					
	35	40	45			
25	Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala					
	50	55	60			
	Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile					
	65	70	75	80		
30	Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe					
	85	90	95			
	Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys					
	100	105	110			
	Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln					

115 120 125

Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val
130 135 140

5 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145 150 155 160

Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
165 170 175

Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180 185 190

10 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
195 200 205

Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
210 215 220

15 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
225 230 235 240

Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
245 250 255

Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
260 265 270

20 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
275 280 285

Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
290 295 300

25 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
305 310 315 320

Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
325 330 335

Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
340 345 350

30 (26) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCCAGGAA ACGCCACCCC AGTGACCACC ACTGCCCCGT GGGCCTCCCT GGGCCTCTCC 60
 GCCAAGACCT GCAACAAACGT GTCCTTCGAA GAGAGCAGGA TAGTCCTGGT CGTGGTGTAC 120
 AGCGCGGTGT GCACGCTGGG GGTGCCGGCC AACTGCCTGA CTGCGTGGCT GGCGCTGCTG 180
 5 CAGGTACTGC AGGGCAACGT GCTGGCCGTC TACCTGCTCT GCCTGGCACT CTGCGAACTG 240
 CTGTACACAG GCACGCTGCC ACTCTGGTC ATCTATATCC GCAACCAGCA CCGCTGGACC 300
 CTAGGCCTGC TGGCCTCGAA GGTGACCGCC TACATCTTCT TCTGCAACAT CTACGTCAGC 360
 ATCCTCTTCC TGTGCTGCAT CTCCTGCGAC CGCTTCGTGG CCGTGGTGTAC CGCGCTGGAG 420
 AGTCGGGGCC GCCGCCGCCG GAGGACCGCC ATCCTCATCT CCGCCTGCAT CTTCATCCTC 480
 10. GTCGGGATCG TTCACTACCC GGTGTTCCAG ACGGAAGACA AGGAGACCTG CTTTGACATG 540
 CTGCAGATGG ACAGCAGGAT TGCCGGGTAC TACTACGCCA GGTTCACCGT TGGCTTGCC 600
 ATCCCTCTCT CCATCATCGC CTTCACCAAC CACCGGATTT TCAGGAGCAT CAAGCAGAGC 660
 ATGGGCTTAA GCGCTGCCCA GAAGGCCAAG GTGAAGCACT CGGCCATCGC GGTGGTTGTC 720
 ATCTTCCTAG TCTGCTTCGC CCCGTACAC CTGGTTCTCC TCGTCAAAGC CGCTGCCTTT 780
 15. TCCTACTACA GAGGAGACAG GAACGCCATG TGCGGCTTGG AGGAAAGGCT GTACACAGCC 840
 TCTGTGGTGT TTCTGTGCCT GTCCACGGTG AACGGCGTGG CTGACCCCAT TATCTACGTG 900
 CTGGCCACGG ACCATTCCCC CCAAGAAAGTG TCCAGAATCC ATAAGGGGTG GAAAGAGTGG 960
 TCCATGAAGA CAGACGTCAC CAGGCTCACC CACAGCAGGG ACACCGAGGA GCTGCAGTCG 1020
 CCCGTGGCCC TTGCAGACCA CTACACCTTC TCCAGGCCCG TGCACCCACC AGGGTCACCA 1080
 20. TGCCCTGCAA AGAGGCTGAT TGAGGAGTCC TGCTGA 1116

(28) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Pro	Gly	Asn	Ala	Thr	Pro	Val	Thr	Thr	Thr	Ala	Pro	Trp	Ala	Ser
1	5													15	

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser
 20 25 30

Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val
 35 40 45

5 Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln
 50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu
 65 70 75 80

10 Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln
 85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile
 100 105 110

Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser
 115 120 125

15 Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg
 130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu
 145 150 155 160

20 Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr
 165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr
 180 185 190

Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe
 195 200 205

25 Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser
 210 215 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val
 225 230 235 240

30 Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
 245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly
 260 265 270

Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser
 275 280 285

35 Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp
 290 295 300

	His	Ser	Arg	Gln	Glu	Val	Ser	Arg	Ile	His	Lys	Gly	Trp	Lys	Glu	Trp
305						310				315				320		
	Ser	Met	Lys	Thr	Asp	Val	Thr	Arg	Leu	Thr	His	Ser	Arg	Asp	Thr	Glu
						325				330				335		
5	Glu	Leu	Gln	Ser	Pro	Val	Ala	Leu	Ala	Asp	His	Tyr	Thr	Phe	Ser	Arg
						340			345				350			
	Pro	Val	His	Pro	Pro	Gly	Ser	Pro	Cys	Pro	Ala	Lys	Arg	Leu	Ile	Glu
						355			360				365			
10	Glu	Ser	Cys													
			370													

(28) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

	ATGGCGAACT ATAGCCATGC AGCTGACAAC ATTTTGCAAA ATCTCTGCC TCTAACAGCC	60
20	TTTCTGAAAC TGACTTCCTT GGGTTTCATA ATAGGAGTCA GCGTGGTGGG CAACCTCCTG	120
	ATCTCCATTT TGCTAGTGAA AGATAAGACC TTGCATAGAG CACCTTACTA CTTCTGTTG	180
	GATCTTGCT GTTCAGATAT CCTCAGATCT GCAATTGTT TCCCATTGTT GTTCAACTCT	240
	GTCAAAAATG GCTCTACCTG GACTTATGGG ACTCTGACTT GCAAAGTGAT TGCCTTCTG	300
	GGGGTTTGT CCTGTTCCA CACTGCTTTC ATGCTTTCT GCATCAGTGT CACCAGATAC	360
25	TTAGCTATCG CCCATCACCG CTTCTATACA AAGAGGCTGA CCTTTGGAC GTGTCTGGCT	420
	GTGATCTGTA TGGTGTGGAC TCTGCTGTG GCCATGGCAT TTCCCCGGT TTTAGACGTG	480
	GGCACTTACT CATTCAATTAG GGAGGAAGAT CAATGCACCT TCCAACACCG CTCCCTCAGG	540
	GCTAATGATT CCTTAGGATT TATGCTGCTT CTTGCTCTCA TCCTCCTAGC CACACAGCTT	600
	GTCTACCTCA AGCTGATATT TTTCGTCCAC GATCGAAGAA AAATGAAGCC AGTCCAGTTT	660
30	GTAGCAGCAG TCAGCCAGAA CTGGACTTTT CATGGTCCTG GAGCCAGTGG CCAGGCAGCT	720
	GCCAATTGGC TAGCAGGATT TGGAAGGGT CCCACACCAC CCACCTTGCT GGGCATCAGG	780
	CAAAATGCAA ACACCACAGG CAGAAGAAGG CTATTGGTCT TAGACCGAGTT CAAAATGGAG	840

AAAAGAATCA	GCAGAATGTT	CTATATAATG	ACTTTCTGT	TTCTAACCTT	GTGGGGCCCC	900
TACCTGGTGG	CCTGTTATTG	GAGAGTTTT	GCAAGAGGGC	CTGAGTAC	AGGGGGATTT	960
CTAACAGCTG	CTGTCTGGAT	GAGTTTGCC	CAAGCAGGAA	TCAATCCTT	TGTCTGCATT	1020
TTCTCAAACA	GGGAGCTGAG	GCGCTGTTTC	AGCACAAACCC	TTCTTACTG	CAGAAAATCC	1080
5	AGGTTACCAA	GGGAACCTTA	CTGTGTTATA	TGA		1113

(29) INFORMATION FOR SEQ ID NO:28:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

15	Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser	1	5	10	15
	Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly	20	25		30
	Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp	35	40		45
20	Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys	50	55	60	
	Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser	65	70	75	80
25	Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val	85		90	95
	Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu	100		105	110
	Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe	115	120		125
30	Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met	130	135	140	
	Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val	145	150	155	160
	Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His				

	165	170	175
	Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala		
	180	185	190
5	Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe		
	195	200	205
	Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val		
	210	215	220
	Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala		
	225	230	235
10	Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu		
	245	250	255
	Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu		
	260	265	270
15	Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr		
	275	280	285
	Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala		
	290	295	300
	Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe		
	305	310	315
20	Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro		
	325	330	335
	Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr		
	340	345	350
25	Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys		
	355	360	365
	Val Ile		
	370		

(30) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGCAGGTCC CGAACAGCAC CGGCCGGAC AACGCGACGC TGCAGATGCT GCGGAACCCG

60

120	GCAGATCGCGG TGGCCCTGCC CGTGGTGTAC TCGCTGGTGG CGGCGGTCA G CATCCCGGGC
180	AACCTCTTCT CTCTGTGGT GCTGTGCCGG CGCATGGGC CCAGATCCCC GTCGGTCATC
240	TTCATGATCA ACCTGAGCGT CACGGACCTG ATGCTGGCCA GCGTGTGCCCC TTTCAAATC
300	TACTACCATT GCAACCGCCA CCACCTGGTA TTCGGGGTGC TGCTTGCAA CGTGGTGACC
360	5 GTGGCCTTT ACGCAAACAT GTATTCCAGC ATCCTCACCA TGACCTGTAT CAGCGTGGAG
420	CGCTTCCTGG GGGTCCTGTA CCCGCTCAGC TCCAAGCGCT GGCGCCGCCG TCGTTACGCG
480	GTGGCCGCGT GTGCAGGGAC CTGGCTGCTG CTCCTGACCG CCCTGTGCCG GCTGGCGCGC
540	ACCGATCTCA CCTACCCGGT GCACGCCCTG GGCATCATCA CCTGCTTCGA CGTCCTCAAG
600	TGGACGATGC TCCCCAGCGT GGCCATGTGG GCCGTGTTCC TCTTCACCAT CTTCATCCTG
660	10 CTGTTCTCA TCCCCTTCGT GATCACCGTG GCTTGTACA CGGCCACCAT CCTCAAGCTG
720	TTGCGCACGG AGGAGGCGCA CGGCCGGGAG CAGCGGAGGC GCGCGGTGGG CCTGGCCGCG
780	GTGGCTTGC TGGCCTTGT CACCTGCTTC GCCCCAAACA ACTTCGTGCT CCTGGCGCAC
840	ATCGTGAGCC GCCTGTTCTA CGGCAAGAGC TACTACCACG TGTACAAGCT CACGCTGTGT
900	CTCAGCTGCC TCAACAACTG TCTGGACCCG TTTGTTTATT ACTTTGCGTC CGGGAAATTC
960	15 CAGCTGCGCC TGCAGGAATA TTTGGGCTGC CGCCGGGTGC CCAGAGACAC CCTGGACACG
1020	CGCCGCGAGA GCCTCTTCTC CGCCAGGACC ACGTCCGTGC GCTCCGAGGC CGGTGCGCAC
1080	CCTGAAGGGA TGGAGGGAGC CACCAGGCCG GGCTCCAGA GGCAGGAGAG TGTGTTCTGA

(31) INFORMATION FOR SEQ ID NO:30:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

1	Met	Gln	Val	Pro	Asn	Ser	Thr	Gly	Pro	Asp	Asn	Ala	Thr	Leu	Gln	Met
5														10		15
20	Leu	Arg	Asn	Pro	Ala	Ile	Ala	Val	Ala	Leu	Pro	Val	Val	Tyr	Ser	Leu
25														30		

30 Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu

	Cys Arg	Arg	Met Gly Pro Arg Ser Pro Ser	Ile Phe Met Ile Asn
	50		55	60
5	Leu Ser Val Thr Asp	Leu Met Leu Ala Ser Val	Leu Pro Phe Gln Ile	
	65	70	75	80
	Tyr Tyr His Cys Asn Arg His His	Trp Val Phe Gly Val	Leu Cys	
	85	90	95	
	Asn Val Val Thr Val Ala Phe	Tyr Ala Asn Met Tyr Ser	Ser Ile Leu	
	100	105	110	
10	Thr Met Thr Cys Ile Ser Val	Glu Arg Phe Leu Gly Val	Leu Tyr Pro	
	115	120	125	
	Leu Ser Ser Lys Arg Trp Arg Arg Arg	Tyr Ala Val Ala Ala	Cys	
	130	135	140	
15	Ala Gly Thr Trp Leu Leu Leu	Thr Ala Leu Cys Pro	Leu Ala Arg	
	145	150	155	160
	Thr Asp Leu Thr Tyr Pro Val His	Ala Leu Gly Ile Ile	Thr Cys Phe	
	165	170	175	
	Asp Val Leu Lys Trp Thr Met Leu	Pro Ser Val Ala Met	Trp Ala Val	
	180	185	190	
20	Phe Leu Phe Thr Ile Phe Ile	Leu Phe Leu Ile Pro	Phe Val Ile	
	195	200	205	
	Thr Val Ala Cys Tyr Thr Ala	Thr Ile Leu Lys	Leu Leu Arg Thr Glu	
	210	215	220	
25	Glu Ala His Gly Arg Glu Gln	Arg Arg Ala Val	Gly Leu Ala Ala	
	225	230	235	240
	Val Val Leu Leu Ala Phe Val	Thr Cys Phe Ala Pro	Asn Asn Phe Val	
	245	250	255	
	Leu Leu Ala His Ile Val Ser	Arg Leu Phe Tyr Gly	Lys Ser Tyr Tyr	
	260	265	270	
30	His Val Tyr Lys Leu Thr	Leu Cys Leu Ser	Cys Leu Asn Asn	Cys Leu
	275	280	285	
	Asp Pro Phe Val Tyr Tyr	Phe Ala Ser Arg	Glu Phe Gln Leu Arg	Leu
	290	295	300	
35	Arg Glu Tyr Leu Gly Cys	Arg Arg Val Pro	Arg Asp Thr Leu Asp	Thr
	305	310	315	320
	Arg Arg Glu Ser Leu Phe Ser	Ala Arg Thr Thr	Ser Val Arg Ser	Glu
	325	330	335	

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350

Gln Arg Gln Glu Ser Val Phe
 355

5 (32) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGAGCGTC	CCTGGGAGGA	CAGCCCAGGC	CCGGAGGGGG	CAGCTGAGGG	CTCGCCTGTG	60	
CCAGTCGCCG	CCGGGGCGCG	CTCCGGTGCC	GCGGCGAGTG	GCACAGGCTG	GCAGCCATGG	120	
15	GCTGAGTGCC	CGGGACCCAA	GGGGAGGGGG	CAACTGCTGG	CGACCGCCGG	CCCTTTGCGT	180
	CGCTGGCCCG	CCCCCTCGCC	TGCCAGCTCC	AGCCCCGCC	CCGGAGCGGC	GTCCGCTCAC	240
	TCGGTTCAAG	GCAGCGCGAC	TGCGGGTGGC	GCACGACCAG	GGCGCAGACC	TTGGGGCGCG	300
	CGGCCCATGG	AGTCGGGGCT	GCTGCGGCCG	GCGCCGGTGA	GCGAGGTCAT	CGTCCTGCAT	360
	TACAAC TACA	CCGGCAAGCT	CCGCGGTGCG	AGCTACCAGC	CGGGTGCCGG	CCTGCGCGCC	420
20	GACGCCGTGG	TGTGCCTGGC	GGTGTGCGCC	TTCATCGTGC	TAGAGAATCT	AGCCGTGTTG	480
	TTGGTGCTCG	GACGCCACCC	GCGCTTCCAC	GCTCCCATGT	TCCTGCTCCT	GGGCAGCCTC	540
	ACGTTGTCGG	ATCTGCTGGC	AGGCGCCGCC	TACGCCGCCA	ACATCCTACT	GTCGGGGCCG	600
	CTCACGCTGA	AACTGTCCCC	CGCGCTCTGG	TTCGCACGGG	AGGGAGGCGT	CTTCGTGGCA	660
	CTCACTGCGT	CCGTGCTGAG	CCTCCTGGCC	ATCGCGCTGG	AGCGCAGCCT	CACCATGGCG	720
25	CGCAGGGGGC	CCGCGCCCGT	CTCCAGTCGG	GGGCGCACGC	TGGCGATGGC	AGCCGCGGCC	780
	TGGGGCGTGT	CGCTGCTCCT	CGGGCTCCTG	CCAGCGCTGG	GCTGGAATTG	CCTGGGTCGC	840
	CTGGACGCTT	GCTCCACTGT	CTTGCCTGTC	TACGCCAAGG	CCTACGTGCT	CTTCTGCGTG	900
	CTCGCCTTCG	TGGGCATCCT	GGCCGCGATC	TGTGCACTCT	ACGCGCGCAT	CTACTGCCAG	960
	GTACGCGCCA	ACGCGCGGCG	CCTGCCGGCA	CGGCCCGGGA	CTGCGGGGAC	CACCTCGACC	1020
30	CGGGCGCGTC	GCAAGCCGCG	CTCTCTGGCC	TTGCTGCGCA	CGCTCAGCGT	GGTGCTCCTG	1080

GCCTTTGTGG CATGTTGGGG CCCCCCTCTTC CTGCTGCTGT TGCTCGACGT GGCGTGCCCCG 1140
 GCGCGCACCT GTCCTGTACT CCTGCAGGCC GATCCCTTCC TGGGACTGGC CATGGCCAAC 1200
 TCACCTTCTGA ACCCCATCAT CTACACGCTC ACCAACCGCG ACCCTGCGCCA CGCGCTCCTG 1260
 CGCCTGGTCT GCTGCGGACG CCACTCCTGC GGCAGAGACC CGAGTGGCTC CCAGCAGTCG 1320
 5 GCGAGCGCGG CTGAGGCTTC CGGGGGCCTG CGCCGCTGCC TGCCCCCGGG CCTTGATGGG 1380
 AGCTTCAGCG GCTCGGAGCG CTCATCGCCC CAGCGCGACG GGCTGGACAC CAGCGGCTCC 1440
 ACAGGCAGCC CCGGTGCACC CACAGCCGCC CGGACTCTGG TATCAGAACCC GGCTGCAGAC 1500
 TGA 1503

(33) INFORMATION FOR SEQ ID NO:32:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu
 1 5 10 15

Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala
 20 25 30

Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly
 35 40 45

Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala
 50 55 60

25 Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His
 65 70 75 80

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg
 85 90 95

30 Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro
 100 105 110

Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg
 115 120 125

Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val
 130 135 140

Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu
145 150 155 160

Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu
165 170 175

5 Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala
180 185 190

Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala
195 200 205

Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser
10 210 215 220

Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala
225 230 235 240

Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met
245 250 255

15 Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala
260 265 270

Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu
275 280 285

Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val
20 290 295 300

Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln
305 310 315 320

Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly
325 330 335

25 Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu
340 345 350

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro
355 360 365

Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys
30 370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn
385 390 395 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg
405 410 415

35 His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg
420 425 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Glu Ala Ser Gly

435

440

445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly
 450 455 460

5 Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser
 465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu
 485 490 495

Pro Ala Ala Asp
 500

10 (34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGCAAGCCG TCGACAATCT CACCTCTGCG CCTGGGAACA CCAGTCTGTG CACCAGAGAC	60
TACAAAATCA CCCAGGTCTCT CTTCCCCTG CTCTACACTG TCCTGTTTT TGTTGGACTT	120
20 ATCACAAATG GCCTGGCGAT GAGGATTTTC TTTCAAATCC GGAGTAAATC AAACTTTATT	180
ATTTTCTTA AGAACACAGT CATTCTGAT CTTCTCATGA TTCTGACTTT TCCATTCAA	240
ATTCTTAGTG ATGCCAAACT GGGAACAGGA CCACTGAGAA CTTTGTGTG TCAAGTTACC	300
TCCGTCATAT TTTATTCAC AATGTATATC AGTATTCAT TCCTGGACT GATAACTATC	360
GATCGCTACC AGAAGACCA CAGGCCATTT AAAACATCCA ACCCCCCAAA TCTCTGGGG	420
25 GCTAAGATTC TCTCTGTTGT CATCTGGCA TTCATGTTCT TACTCTCTT GCCTAACATG	480
ATTCTGACCA ACAGGCAGCC GAGAGACAAG AATGTGAAGA AATGCTCTT CCTTAAATCA	540
GAGTCGGTC TAGTCTGGCA TGAAATAGTA AATTACATCT GTCAAGTCAT TTTCTGGATT	600
AATTCTTAA TTGTTATTGT ATGTTATACA CTCATTACAA AAGAACTGTA CCGGTCATAC	660
GTAAGAACGA GGGGTGTAAG TAAAGCCCC AGGAAAAAGG TGAACGTCAA AGTTTCATT	720
30 ATCATTGCTG TATTCTTAT TTGTTTGTT CCTTCCATT TTGCCGAAT TCCTTACACC	780
CTGAGCCAAA CCCGGGATGT CTTTGACTGC ACTGCTGAAA ATACTCTGTT CTATGTGAAA	840

GAGAGCACTC TGTGGTTAAC TTCCTTAAAT GCATGCCTGG ATCCGTTCAT CTATTTTTC 900
 CTTTGCAAGT CCTTCAGAAA TTCCTGATA AGTATGCTGA AGTGGCCCAA TTCTGCAACA 960
 TCTCTGTCCC AGGACAATAG GAAAAAAAGAA CAGGATGGTG GTGACCCAAA TGAAGAGACT 1020
 CCAATGTAA 1029

5 (35) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 10 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
 1 5 10 15

15 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
 20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
 35 40 45

20 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
 50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
 65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
 85 90 95

25 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
 100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
 115 120 125

30 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
 130 135 140

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
 145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
 165 170 175

35 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr

	180	185	190
	Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys		
	195	200	205
5	Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg		
	210	215	220
	Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile		
	225	230	235
	Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg		
	245	250	255
10	Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala		
	260	265	270
	Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser		
	275	280	285
15	Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser		
	290	295	300
	Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr		
	305	310	315
	Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro		
	325	330	335
20	Asn Glu Glu Thr Pro Met		
	340		
(36) INFORMATION FOR SEQ ID NO:35:			
	(i) SEQUENCE CHARACTERISTICS:		
25	(A) LENGTH: 1077 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: DNA (genomic)		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:		
30	ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA GACTTCGCGG 60		
	GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG GGCTGCCTGG CAACGGCTTC 120		
	GTGGTGTGGA GCTTGGCGGG CTGGCGGCCT GCACGGGGGC GACCGCTGGC GGCCACGCTT 180		
	GTGCTGCACC TGGCGCTGGC CGACGGCGCG GTGCTGCTGC TCACGCCGCT CTTTGTGGCC 240		
	TTCCTGACCC GGCAGGCCTG GCCGCTGGC CAGGCGGGCT GCAAGGCGGT GTACTACGTG 300		

TGCGCGCTCA	GCATGTACGC	CAGCGTGCTG	CTCACCGGCC	TGCTCAGCCT	GCAGCGCTGC	360	
CTCGCAGTCA	CCCGCCCCCTT	CCTGGCGCCT	CGGCTGCGCA	GCCCCGCCCT	GGCCCGCCGC	420	
CTGCTGCTGG	CGGTCTGGCT	GGCCGCCCTG	TTGCTCGCCG	TCCCGGCCGC	CGTCTACCGC	480	
CACCTGTGGA	GGGACCGCGT	ATGCCAGCTG	TGCCACCCGT	CGCCGGTCCA	CGCCGCCGCC	540	
5	CACCTGAGCC	TGGAGACTCT	GACCGCTTTC	GTGCTTCCTT	TCGGGCTGAT	GCTCGGCTGC	600
TACAGCGTGA	CGCTGGCACG	GCTGCGGGC	GCCCCGCTGGG	GCTCCGGCG	GCACGGGGCG	660	
CGGGTGGGCC	GGCTGGTGAG	CGCCATCGTG	CTTGCCTTCG	GCTTGCTCTG	GGCCCCCTAC	720	
CACGCAGTCA	ACCTTCTGCA	GGCGGTCGCA	GCGCTGGCTC	CACCGGAAGG	GGCCTTGGCG	780	
AAGCTGGCG	GAGCCGGCCA	GGCGCGCGA	GCGGAACTA	CGGCCTTGGC	CTTCTTCAGT	840	
10	TCTAGCGTCA	ACCCGGTGCT	CTACGTCTTC	ACCGCTGGAG	ATCTGCTGCC	CCGGGCAGGT	900
CCCCGTTTCC	TCACGCGGCT	CTTCGAAGGC	TCTGGGGAGG	CCCGAGGGGG	CGGCCGCTCT	960	
AGGGAAGGGA	CCATGGAGCT	CCGAACCTACC	CCTCAGCTGA	AAGTGGTGGG	GCAGGGCCGC	1020	
GGCAATGGAG	ACCCGGGGGG	TGGGATGGAG	AAGGACGGTC	CGGAATGGGA	CCTTTGA	1077	

(37) INFORMATION FOR SEQ ID NO:36:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ser	Val	Cys	Tyr	Arg	Pro	Pro	Gly	Asn	Glu	Thr	Leu	Leu	Ser	Trp	
1															15	
Lys	Thr	Ser	Arg	Ala	Thr	Gly	Thr	Ala	Phe	Leu	Leu	Leu	Ala	Ala	Leu	
25															30	
Leu	Gly	Leu	Pro	Gly	Asn	Gly	Phe	Val	Val	Trp	Ser	Leu	Ala	Gly	Trp	
35															45	
Arg	Pro	Ala	Arg	Gly	Arg	Pro	Leu	Ala	Ala	Thr	Leu	Val	Leu	His	Leu	
50															60	
30	Ala	Leu	Ala	Asp	Gly	Ala	Val	Leu	Leu	Leu	Thr	Pro	Leu	Phe	Val	Ala
65															80	
	Phe	Leu	Thr	Arg	Gln	Ala	Trp	Pro	Leu	Gly	Gln	Ala	Gly	Cys	Lys	Ala

	85	90	95	
	Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr			
	100	105	110	
5	Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu			
	115	120	125	
	Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala			
	130	135	140	
	Val Trp Leu Ala Ala Leu Leu Ala Val Pro Ala Ala Val Tyr Arg			
	145	150	155	160
10	His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val			
	165	170	175	
	His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu			
	180	185	190	
15	Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu			
	195	200	205	
	Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg			
	210	215	220	
	Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr			
	225	230	235	240
20	His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu			
	245	250	255	
	Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly			
	260	265	270	
25	Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr			
	275	280	285	
	Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu			
	290	295	300	
	Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Arg Ser			
	305	310	315	320
30	Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val			
	325	330	335	
	Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Met Glu Lys Asp			
	340	345	350	
35	Gly Pro Glu Trp Asp Leu			
	355			

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGCTGGGGA	TCATGGCATG	GAATGCACT	TGCAAAA	ACT GGCTGGCAGC	AGAGGCTGCC	60
CTGGAAAAGT	ACTACCTTTC	CATTTTTAT	GGGATTGAGT	TCGTTGTGGG	AGTCCTTGGA	120
10 AATACCATTG	TTGTTTACGG	CTACATCTTC	TCTCTGAAGA	ACTGGAACAG	CAGTAATATT	180
TATCTCTTTA	ACCTCTCTGT	CTCTGACTTA	GCTTTCTGT	GCACCCCTCCC	CATGCTGATA	240
AGGAGTTATG	CCAATGGAAA	CTGGATATAT	GGAGACGTGC	TCTGCATAAG	CAACCGATAT	300
GTGCTTCATG	CCAACCTCTA	TACCAGCATT	CTCTTTCTCA	CTTTTATCAG	CATAGATCGA	360
TACTTGATAA	TTAAGTATCC	TTTCCGAGAA	CACCTTCTGC	AAAAGAAAGA	GTTTGCTATT	420
15 TTAATCTCCT	TGGCCATTG	GGTTTTAGTA	ACCTTAGAGT	TACTACCCAT	ACTTCCCCTT	480
ATAAATCCTG	TTATAACTGA	CAATGGCACC	ACCTGTAATG	ATTTGCAAG	TTCTGGAGAC	540
CCCAACTACA	ACCTCATT	AAGCATGTGT	CTAACACTGT	TGGGGTTCC	TATTCCCTTT	600
TTTGTGATGT	GT	TTACAAGATT	GCTCTTTCC	TAAAGCAGAG	GAATAGGCAG	660
GTTGCTACTG	CTCTGCC	TGAAAAGCCT	CTCAACTTGG	TCATCATGGC	AGTGGTAATC	720
20 TTCTCTGTGC	TTTTTACACC	CTATCACGTC	ATGCGGAATG	TGAGGATCGC	TTCACGCC	780
GGGAGTTGGA	AGCAGTATCA	GTGCACTCAG	GTCGTCA	ACTCCTTTA	CATTGTGACA	840
CGGCCTTGG	CCTTCTGAA	CAGTGTCA	AACCCTGTCT	TCTATTTCT	TTTGGGAGAT	900
CACTTCAGGG	ACATGCTGAT	GAATCAACTG	AGACACAACT	TCAAATCCCT	TACATCCTT	960
AGCAGATGGG	CTCATGAACT	CCTACTTCA	TTCAGAGAAA	AGTGA		1005

25 (39) INFORMATION FOR SEQ ID NO:38:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala
1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile
5 20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr
35 40 45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn
50 55 60

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile
10 65 70 75 80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile
15 85 90 95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe
100 105 110

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe
115 120 125

Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu
130 135 140

Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu
20 145 150 155 160

Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala
165 170 175

Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr
25 180 185 190

Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr
195 200 205

Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala
210 215 220

Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
30 225 230 235 240

Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
245 250 255

Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
35 260 265 270

Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser

275

280

285

Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
 290 295 300

5 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
 305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Ser Phe Arg Glu Lys
 325 330

(40) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGCAGGCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAAACCTG	60
ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG	120
CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC	180
TTTGGCAATG CTCTGGTGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC	240
20 AACATCTTAA TCTGCTCCTT GGCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC	300
GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG	360
GTGCCATTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT	420
GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA	480
AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG	540
25 TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC	600
TGCTTAGAAC AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC	660
ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA	720
CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA	780
ATGTCCAAAA TAGCCAGGAA GAAGAACGA GCTGTCATTA TGATGGTGAC AGTGGTGGCT	840
30 CTCTTTGCTG TGTGCTGGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT	900
TTTGAAAAGG AATATGATGA TGTACACAATC AAGATGATT TTGCTATCGT GCAAATTATT	960

GGATTTCCA	ACTCCATCTG	TAATCCATT	GTCTATGCAT	TTATGAATGA	AAACTTCAA	1020	
AAAAATGTTT	TGTCTGCAGT	TTGTTATTGC	ATAGTAAATA	AAACCTTCTC	TCCAGCACAA	1080	
AGGCATGGAA	ATTCAGGAAT	TACAATGATG	CGGAAGAAAG	CAAAGTTTC	CCTCAGAGAG	1140	
AATCCAGTGG	AGGAAACCAA	AGGAGAAGCA	TTCAGTGATG	GCAACATTGA	AGTCAAATTG	1200	
5	TGTGAACAGA	CAGAGGAGAA	GAAAAAGCTC	AAACGACATC	TTGCTCTCTT	TAGGTCTGAA	1260
	CTGGCTGAGA	ATTCTCCTTT	AGACAGTGGG	CATTAA		1296	

(41) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 431 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

15	Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg					
	1	5	10	15		
	Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg					
	20	25	30			
20	Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu					
	35	40	45			
	Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala					
	50	55	60			
	Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr					
	65	70	75	80		
25	Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe					
	85	90	95			
	Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu					
	100	105	110			
30	Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala					
	115	120	125			
	Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His					
	130	135	140			
	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg					
	145	150	155	160		

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
 165 170 175
 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
 180 185 190
 5 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
 195 200 205
 Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
 210 215 220
 10 Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu
 225 230 235 240
 Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
 245 250 255
 His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Arg Ala Val
 260 265 270
 15 Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro
 275 280 285
 Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu
 290 295 300
 20 Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile
 305 310 315 320
 Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn
 325 330 335
 Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
 340 345 350
 25 Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr
 355 360 365
 Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
 370 375 380
 Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
 385 390 395 400
 30 Cys Glu Gln Thr Glu Glu Lys Lys Leu Lys Arg His Leu Ala Leu
 405 410 415
 Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
 420 425 430

35 (42) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGTGTACAG CAGTTCGCAG AGTG

24

(43) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

15 GAGTGCCAGG CAGAGCAGGT AGAC

24

(44) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

25 CCCGAATTCC TGCTTGCTCC CAGCTTGGCC C

31

(45) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTGGATCCT GCTGTCAAAG GTCCCATTCC GG

32

(46) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACAATGCT AGGTGTGGTC

20

(47) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGCATAGACA ATGGGATTAC AG

22

(48) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCACAATGCT AGGTGTGGTC TGGCTGGTGG CAGTCATCGT AGGATCACCC ATGTGGCACG

60

TGCAACAACT TGAGATCAAA TATGACTTCC TATATGAAAA GGAACACATC TGCTGCTTAG

120

AAGAGTGGAC CAGCCCTGTG CACCAAGA TCTACACCAC CTTCATCCTT GTCATCCTCT 180
TCCTCCTGCC TCTTATGGTG ATGCTTATTG TGTACGTAAA ATTGGTTATG AACTTTGGAT 240
AAAGAAAAAGA GTTGGGGATG GTTCAGTGCT TCGAACTATT CATGGAAAAG AAATGTCAA 300
AATAGCCAGG AAGAAGAAC GAGCTGTCA TATGATGGTG ACAGTGGTGG CTCTCTTGC 360
5 TGTGTGCTGG GCACCATTCC ATGTTGTCCA TATGATGATT GAATACAGTA ATTTTGAAAA 420
GGAATATGAT GATGTCACAA TCAAGATGAT TTTGCTATC GTGCAAATTA TTGGATTTTC 480
CAACTCCATC TGTAATCCCA TTGTCTATGC A 511

(49) INFORMATION FOR SEQ ID NO:48:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGCTTAGAA GAGTGGACCA G

21

(50) INFORMATION FOR SEQ ID NO:49:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGTGCACCA GAAGATCTAC AC

22

(51) INFORMATION FOR SEQ ID NO:50:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAGGATGAA GGTGGTGTAG A

21

5 (52) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGTAGATCT TCTGGTGCAC AGG

23

15 (53) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCAATGCAGG TCATAGTGAG C

21

(54) INFORMATION FOR SEQ ID NO:53:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGGAGCATGG TGACGGGAAT GCAGAAG

27

(55) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTGATGAGCA GGTCACTGAG CGCCAAG

27

(56) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCAATGCAGG CGCTTAACAT TAC

23

(57) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTGGGTTACA ATCTGAAGGG CA

22

(58) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

10 ACTCCGTGTC CAGCAGGACT CTG

23

(58) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

20 TGC GTGTTCC TGGACCCCTCA CGTG

24

(58) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30 CAGGCCTTGG ATTTTAATGT CAGGGATGG

29

(61) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

5 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGAGAGTCAG CTCTGAAAGA ATTCAGG

27

(62) INFORMATION FOR SEQ ID NO:61:

- 10 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGATGTGATG CCAGATACTA ATAGCAC

27

(63) INFORMATION FOR SEQ ID NO:62:

- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCTGATTTCAT TTAGGTGAGA TTGAGAC

27

(64) INFORMATION FOR SEQ ID NO:63:

- 30 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(3) INFORMATION FOR SEQ ID NO:63:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTGGATCCA CATAATGCAT TTTCTC

26

(66) INFORMATION FOR SEQ ID NO:65:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCCAA

60

GCTGGAAGGC ATAATTACAT ATTTGTCTACG ATTCCTACTT TATACAGTAT CATCTTGTC

120

GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATT ACTTTTATAT GAAGCTGAAG

180

ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACTGGCTG ACTTATGCTT TTTACTGACT

240

25 TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTGG CAATTACCTA

300

TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCACG

360

TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC

420

ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGGCCAGT

480

TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTGT

540

30 GCTTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGCCT GACCAAAAT

600

ATACTGGGTT	TCCTGTTCC	TTTCTGATC	ATTCTTACAA	GTTATACTCT	TATTTGGAAG	660	
GCCCTAAAGA	AGGCTTATGA	AATTCAAG	AACAAACCAA	GAAATGATGA	TATTTTAAG	720	
ATAATTATGG	CAATTGTGCT	TTTCTTTTC	TTTCCTGGA	TTCCCCACCA	AATATTCACT	780	
TTTCTGGATG	TATTGATTCA	ACTAGGCATC	ATACGTGACT	GTAGAATTGC	AGATATTGTG	840	
5	GACACGGCCA	TGCCTATCAC	CATTTGTATA	GCTTATTTA	ACAATTGCCT	GAATCCTCTT	900
TTTTATGGCT	TTCTGGGAA	AAAATTAAA	AGATATTTC	TCCAGCTCT	AAAATATATT	960	
CCCCCAAAAG	CCAAATCCCA	CTCAAACCTT	TCAACAAAAA	TGAGCACGCT	TTCCCTACCGC	1020	
CCCTCAGATA	ATGTAAGCTC	ATCCACCAAG	AAGCCTGCAC	CATGTTTGA	GGTTGAGTGA	1080	

(67) INFORMATION FOR SEQ ID NO:66:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Ile	Leu	Asn	Ser	Ser	Thr	Glu	Asp	Gly	Ile	Lys	Arg	Ile	Gln	Asp	
1																
							5						10		15	
Asp	Cys	Pro	Lys	Ala	Gly	Arg	His	Asn	Tyr	Ile	Phe	Val	Met	Ile	Pro	
20																
							20				25			30		
Thr	Leu	Tyr	Ser	Ile	Ile	Phe	Val	Val	Gly	Ile	Phe	Gly	Asn	Ser	Leu	
35																
							35				40		45			
Val	Val	Ile	Val	Ile	Tyr	Phe	Tyr	Met	Lys	Leu	Lys	Thr	Val	Ala	Ser	
50																
							50				55		60			
25	Val	Phe	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Cys	Phe	Leu	Leu	Thr
	65					70						75			80	
Leu	Pro	Leu	Trp	Ala	Val	Tyr	Thr	Ala	Met	Glu	Tyr	Arg	Trp	Pro	Phe	
	85					90							95			
30	Gly	Asn	Tyr	Leu	Cys	Lys	Ile	Ala	Ser	Ala	Ser	Val	Ser	Phe	Asn	Leu
	100										105			110		
Tyr	Ala	Ser	Val	Phe	Leu	Leu	Thr	Cys	Leu	Ser	Ile	Asp	Arg	Tyr	Leu	
	115					120							125			
Ala	Ile	Val	His	Pro	Met	Lys	Ser	Arg	Leu	Arg	Arg	Thr	Met	Leu	Val	

130 135 140
 Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
 145 150 155 160
 Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
 5 165 170 175
 Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
 180 185 190
 Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
 195 200 205
 10 Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
 210 215 220
 Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
 225 230 235 240
 Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His
 15 245 250 255
 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
 260 265 270
 Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
 275 280 285
 20 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
 290 295 300
 Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
 305 310 315 320
 Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
 25 325 330 335
 Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
 340 345 350
 Ala Pro Cys Phe Glu Val Glu
 355
 30 (68) INFORMATION FOR SEQ ID NO:67:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACCATGGGCA GCCCCTGGAA CGGCAGC

27

(69) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGAACACCACCA CCAGCAGGAC GCGGACGGTC TGCCGGTGG

39

(70) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

20 GTCCGCGTCC TGCTGGTGGT GGTTCTGGCA TTTATAATT

39

(71) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CCTGGATCCT TATCCCATCG TCTTCACGTT AGC

33

30 (72) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

5 CTGGAATTCT CCTGCCAGCA TGGTGA

26

(73) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCAGGATCCT ATATTGCGTG CTCTGTCCCC

30

(74) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGTGAAC CCACCCACCG TGGGATGCAC ACTTCTCTGC ACCTCTGGAA CCGCAGCAGT

60

TACAGACTGC ACAGCAATGC CAGTGAGTCC CTTGGAAAAG GCTACTCTGA TGGAGGGTGC

120

TACGAGCAAC TTTTGTCCTC TCCTGAGGTG TTTGTGACTC TGGGTGTCAT CAGCTTGTG

180

GAGAATATCT TAGTGATTGT GGCAATAGCC AAGAACAAAGA ATCTGCATTC ACCCATGTAC

240

30 TTTTCATCT GCAGCTTGGC TGTGGCTGAT ATGCTGGTGA GCGTTCAAA TGGATCAGAA

300

ACCATTATCA TCACCCATTAAACAGTACA GATACGGATG CACAGAGTTT CACAGTGAAT

360

ATTGATAATG TCATTGACTC GGTGATCTGT AGCTCCTTGC TTGCATCCAT TTGCAGCCTG

420

CTTTCAATTG CAGTGGACAG GTACTTTACT ATCTTCTATG CTCTCCAGTA CCATAACATT	480
ATGACAGTTA AGCGGGTTGG GATCAGCATA AGTTGTATCT GGGCAGCTTG CACGGTTCA	540
GGCATTGGT TCATCATTAA CTCAGATAGT AGTGCTGTCA TCATCTGCCT CATCACCATG	600
TTCTTCACCA TGCTGGCTCT CATGGCTTCT CTCTATGTCC ACATGTTCCCT GATGGCCAGG	660
5 CTTCACATTA AGAGGATTGC TGTCCCTCCC GGCACGGTG CCATCCGCCA AGGTGCCAAT	720
ATGAAGGGAG CGATTACCTT GACCATCCTG ATTGGCGTCT TTGTTGTCTG CTGGGCCCA	780
TTCTTCCTCC ACTTAATATT CTACATCTCT TGTCCCTCAGA ATCCATATTG TGTGTGCTTC	840
ATGTCTCACT TTAACTTGTA TCTCATACTG ATCATGTGTA ATTCAATCAT CGATCCTCTG	900
ATTATATGCAC TCCGGAGTCAGAAACTGAGG AAAACCTTCA AAGAGATCAT CTGTTGCTAT	960
10 CCCCTGGGAG GCCTTTGTGA CTTGTCTAGC AGATATTAA	999

(75) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp	
20 1 5 10 15	15
Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly	
25 20 25 30	30
Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro	
35 35 40 45	45
25 Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu	
50 50 55 60	60
Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr	
65 65 70 75 80	80
30 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser	
85 85 90 95	95
Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr	
100 100 105 110	110
Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val	

	115	120	125
	Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala		
	130	135	140
5	Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile		
	145	150	155
	Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala		
	165	170	175
	Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala		
	180	185	190
10	Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met		
	195	200	205
	Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys		
	210	215	220
15	Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn		
	225	230	235
	Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val		
	245	250	255
	Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro		
	260	265	270
20	Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu		
	275	280	285
	Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu		
	290	295	300
25	Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr		
	305	310	315
	Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr		
	325	330	

(76) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGAAGCTTC GAGCTGAGTA AGGCGGCCGGG CT

(77) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTGGAATTCA TTTGCCCTGC CTCAACCCCC A

31

10 (78) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGAGCTGC TAAAGCTGAA CCGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC	60
CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG	120
20 CCCCCCTCGCA TTCGGGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT	180
TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTGGGA	240
CTGAGCCGCC GCCTGAGGAC TGTCACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC	300
CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTC	360
ATCTTTGGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG	420
25 TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACTG	480
CAGGCACGAG TGTGGCAGAC GCGCTCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG	540
CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT	600
CGTGTGCTGC AGTGCCTGCA TCGCTGGCCC AGTGCCTGGG TCCGCCAGAC CTGGTCCGTA	660
CTGCTGCTTC TGCTCTTGTGTT CTTCATCCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT	720
30 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTTGACGGCG ACAGTGACAG CGACAGCCAA	780
AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTG ACCAGAACGG GCGTTGCCGG	840

CCTGAGACTG GCGCGGTTGG CAAAGACAGC GATGGCTGCT ACGTGCAACT TCCACGTTCC 900
 CGGCCTGCCCG TGGAGCTGAC GGCGCTGACG GCTCCTGGGC CGGGATCCGG CTCCCGGCC 960
 ACCCAGGCCA AGCTGCTGGC TAAGAAGCGC GTGGTGCAGA TGTTGCTGGT GATCGTTGTG 1020
 CTTTTTTTTC TGTGTTGGTT GCCAGTTAT AGTGCCAACA CGTGGCGCGC CTTTGATGGC 1080
 5 CCGGGTGCAC ACCGAGCACT CTCGGGTGCT CCTATCTCCT TCATTCACCT GCTGAGCTAC 1140
 GCCTCGGCCT GTGTCAACCC CCTGGTCTAC TGCTTCATGC ACCGTCGCTT TCGCCAGGCC 1200
 TGCCTGGAAA CTTGCGCTCG CTGCTGCCAC CGGCCTCCAC GAGCTCGCCC CAGGGCTCTT 1260
 CCCGATGAGG ACCCTCCCAC TCCCTCCATT GCTTCGCTGT CCAGGCTTAG CTACACCACC 1320
 ATCAGCACAC TGGGCCCTGG CTGA 1344

10 (79) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
 1 5 10 15

20 Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
 20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
 35 40 45

25 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
 50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
 65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
 85 90 95

30 Ala Val Ser Asp Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
 100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
 115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
 130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
 145 150 155 160

5 Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
 165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
 180 185 190

10 Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
 195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
 210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
 225 230 235 240

15 Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
 245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
 260 265 270

20 Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys
 275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
 290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
 305 310 315 320

25 Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu
 325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
 340 345 350

30 Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
 355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
 370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala
 385 390 395 400

35 Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
 405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser

420

425

430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
435 440 445

(80) INFORMATION FOR SEQ ID NO:79:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TGCAAGCTTA AAAAGGAAAAA AATGAACAGC

30

(81) INFORMATION FOR SEQ ID NO:80:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TAAGGGATCCC TTCCCTTCAA AACATCCTTG

30

(82) INFORMATION FOR SEQ ID NO:81:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1014 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

30 ATGAACAGCA CATGTATTGA AGAACAGCAT GACCTGGATC ACTATTTGTT TCCCATTGTT

60

TACATCTTG TGATTATAGT CAGCATTCCA GCCAATATTG GATCTCTGTG TGTGTCTTTC

120

CTGCAACCCA AGAAGGAAAG TGAACCTAGGA ATTTACCTCT TCAGTTTGTC ACTATCAGAT

180

TTACTCTATG CATTAACTCT CCCTTATGG ATTGATTATA CTTGGAATAA AGACAACTGG

240

ACTTTCTCTC CTGCCCTGTG CAAAGGGAGT GCTTTCTCA TGTACATGAA GTTTTACAGC 300
 AGCACAGCAT TCCTCACCTG CATTGCCGTT GATCGGTATT TGGCTGTTGT CTACCCTTG 360
 AAGTTTTTT TCCTAAGGAC AAGAAGAATT GCACTCATGG TCAGCCTGTC CATCTGGATA 420
 TTGGAAACCA TCTTCAATGC TGTCATGTTG TGGGAAGATG AAACAGTTGT TGAATATTGC 480
 5 GATGCCGAAA AGTCTAATTT TACTTTATGC TATGACAAAT ACCCTTTAGA GAAATGGCAA 540
 ATCAACCTCA ACTTGTTCAG GACGTGTACA GGCTATGCAA TACCTTTGGT CACCACCTG 600
 ATCTGTAACC GGAAAGTCTA CCAAGCTGTG CGGCACAATA AAGCCACGGA AAACAAGGAA 660
 AAGAAGAGAA TCATAAAACT ACTTGTTCAG ATCACAGTTA CTTTGTCTT ATGCTTTACT 720
 CCCTTCATG TGATGTTGCT GATTGCTGC ATTTAGAGC ATGCTGTGAA CTTCGAAGAC 780
 10 CACAGCAATT CTGGGAAGCG AACTTACACA ATGTATAGAA TCACGGTTGC ATTAACAAGT 840
 TTAAATTGTG TTGCTGATCC AATTCTGTAC TGTTTGTAA CCGAAACAGG AAGATATGAT 900
 ATGTGGAATA TATTAATT CTGCACTGGG AGGTGTAATA CATCACAAAG ACAAAAGAAAA 960
 CGCATACTTT CTGTTCTAC AAAAGATACT ATGGAATTAG AGGTCTTGA GTAG 1014

(83) INFORMATION FOR SEQ ID NO:82:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
 1 5 10 15

Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
 20 25 30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu
 35 40 45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
 50 55 60

30 Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
 65 70 75 80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met

	85	90	95
	Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg		
	100	105	110
5	Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg		
	115	120	125
	Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile		
	130	135	140
	Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys		
	145	150	155
10	Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu		
	165	170	175
	Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr		
	180	185	190
15	Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln		
	195	200	205
	Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile		
	210	215	220
	Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr		
	225	230	235
20	Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val		
	245	250	255
	Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr		
	260	265	270
25	Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile		
	275	280	285
	Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile		
	290	295	300
	Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys		
	305	310	315
30	Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu		
	325	330	335
	Glu		

(84) INFORMATION FOR SEQ ID NO:83:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

5 CAGGAAGAAG AAACGAGCTG TCATTATGAT GGTGACAGTG
40

(85) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

15 CACTGTCACC ATCATAATGA CAGCTCGTTT CTTCTTCCTG
40

(86) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

25 GGCCACCGGGC AGACCAAACG CGTCCTGCTG
30

(87) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T
31

(88) INFORMATION FOR SEQ ID NO:87:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGAAAAGAAG AGAATCAAAA AACTACTTGT CAGCATC

37

(89) INFORMATION FOR SEQ ID NO:88:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

20 CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(90) INFORMATION FOR SEQ ID NO:89:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCCAA 60
30 GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTGTG 120
GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATT ACTTTATAT GAAGCTGAAG 180
ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACTGGCTG ACTTATGCTT TTTACTGACT 240
TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTGG CAATTACCTA 300

TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCACG 360
 TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC 420
 ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGGCCAGT 480
 TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTGT 540
 5 GCTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAT 600
 ATACTGGGTT TCCTGTTCC TTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG 660
 GCCCTAAAGA AGGCTTATGA AATTAGAAG AACAAACCAA GAAATGATGA TATTAAAAAG 720
 ATAATTATGG CAATTGTGCT TTTCTTTTC TTTCTGGA TTCCCCACCA AATATTCACT 780
 TTTCTGGATG TATTGATTCA ACTAGGCATC ATACGTGACT GTAGAATTGC AGATATTGTG 840
 10 GACACGGCCA TGCCTATCAC CATTGTATA GCTTATTTA ACAATTGCCT GAATCCTCTT 900
 TTTTATGGCT TTCTGGGAA AAAATTAAA AGATATTTTC TCCAGCTTCT AAAATATATT 960
 CCCCCAAAAG CCAAATCCCA CTCAAACCTT TCAACAAAAA TGAGCACGCT TTCCTACCGC 1020
 CCCTCAGATA ATGTAAGCTC ATCCACCAAG AAGCCTGCAC CATGTTTGA GGTTGAGTGA 1080

(91) INFORMATION FOR SEQ ID NO:90:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
 25 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
 35 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
 50 55 60

30 Val Phe Leu Leu Asn Leu Ala Asp Leu Cys Phe Leu Leu Thr
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe

	85	90	95
	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu		
	100	105	110
5	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155
10	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
15	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys		
	225	230	235
20	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His		
	245	250	255
	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
	260	265	270
25	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
	275	280	285
	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
	290	295	300
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
	305	310	315
30	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
	325	330	335
	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
	340	345	350
35	Ala Pro Cys Phe Glu Val Glu		
	355		

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CCAAGAAATG ATGATATTAA AAAGATAATT ATGGC

35

(93) INFORMATION FOR SEQ ID NO:92:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(94) INFORMATION FOR SEQ ID NO:93:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCAAA

60

GCTGGAAGGC ATAATTACAT ATTTGTACG ATTCCTACTT TATACAGTAT CATCTTGTG

120

GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG

180

ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACTGGCTG ACTTATGCTT TTTACTGACT

240

30 TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA

300

TGTAAGATTG CTTCAGCCAG CGTCAGTTTC GCCCTGTACG CTAGTGTGTT TCTACTCACG

360

TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC

420

ACAATGCTTG	TAGCCAAAGT	CACCTGCATC	ATCATTGGC	TGCTGGCAGG	CTTGGCCAGT	480
TTGCCAGCTA	TAATCCATCG	AAATGTATTT	TTCATTGAGA	ACACCAATAT	TACAGTTTGT	540
GCTTTCCATT	ATGAGTCCC	AAATTCAACC	CTTCCGATAG	GGCTGGCCT	GACCAAAAT	600
ATACTGGGTT	TCCTGTTCC	TTTCTGATC	ATTCTTACAA	GTTACTCT	TATTTGGAAG	660
5	GCCCTAAAGA	AGGCTTATGA	AATTCAAG	ACAAACCAA	GAAATGATGA	720
ATAATTATGG	CAATTGTGCT	TTTCTTTTC	TTTCCTGGA	TTCCCCACCA	AATATTCACT	780
TTTCTGGATG	TATTGATTCA	ACTAGGCATC	ATACGTGACT	GTAGAATTGC	AGATATTGTG	840
GACACGGCCA	TGCCTATCAC	CATTTGTATA	GCTTATTTA	ACAATTGCCT	GAATCCTCTT	900
TTTTATGGCT	TTCTGGGAA	AAAATTAAA	AGATATTTTC	TCCAGCTTCT	AAAATATATT	960
10	CCCCCAAAAG	CCAAATCCC	CTCAACCTT	TCAACAAAAA	TGAGCACGCT	1020
CCCTCAGATA	ATGTAAGCTC	ATCCACCAAG	AAGCCTGCAC	CATTTTGA	GGTTGAGTGA	1080

(95) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

20	Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp					
	1	5	10	15		
	Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro					
	20	25	30			
25	Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu					
	35	40	45			
	Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser					
	50	55	60			
	Val Phe Leu Leu Asn Leu Ala Asp Leu Cys Phe Leu Leu Thr					
	65	70	75	80		
30	Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe					
	85	90	95			
	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu					

	100	105	110
	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
5	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155
	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
10	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
15	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
	225	230	235
	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His		
	245	250	255
20	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
	260	265	270
	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
	275	280	285
25	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
	290	295	300
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
	305	310	315
	320		
	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
	325	330	335
30	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
	340	345	350
	Ala Pro Cys Phe Glu Val Glu		
	355		

(97) INFORMATION FOR SEQ ID NO:95:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(97) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CCTGCAGGCG AAACTGACTC TGGCTGAAG

29

(98) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGTACGCTA GTGTGTTCT ACTCACGTGT CTCAGCATTG AT

42

(99) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGATCCA CATAATGCAT TTTCTC

26

(100) INFORMATION FOR SEQ ID NO:99:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGATTCTCA	ACTCTTCTAC	TGAAGATGGT	ATTAAAAGAA	TCCAAGATGA	TTGTCCAAA	60	
GCTGGAAGGC	ATAATTACAT	ATTTGTCATG	ATTCCTACTT	TATACAGTAT	CATCTTGTG	120	
GTGGGAATAT	TTGGAAACAG	CTTGGTGGTG	ATAGTCATT	ACTTTTATAT	GAAGCTGAAG	180	
15 ACTGTGGCCA	GTGTTTTCT	TTTGAATT	GA	ACTGGCTG	ACTTATGCTT	TTTACTGACT	240
TTGCCACTAT	GGGCTGTCTA	CACAGCTATG	GAATACCGCT	GGCCCTTG	CAATTACCTA	300	
TGTAAGATTG	CTTCAGCCAG	CGTCAGTTTC	AACCTGTACG	CTAGTGTGTT	TCTACTCACG	360	
TGTCTCAGCA	TTGATCGATA	CCTGGCTATT	GTTCACCCAA	TGAAGTCCCG	CCTTCGACGC	420	
ACAATGCTTG	TAGCCAAAGT	CACCTGCATC	ATCATTGGC	TGCTGGCAGG	CTTGGCCAGT	480	
20 TTGCCAGCTA	TAATCCATCG	AAATGTATTT	TTCATTGAGA	ACACCAATAT	TACAGTTGT	540	
GCTTCCATT	ATGAGTCCC	AAATTCAACC	CTTCCGATAG	GGCTGGCCT	GACCAAAAT	600	
ATACTGGTT	TCCTGTTCC	TTTCTGATC	ATTCTTACAA	GTTATTTGG	AATTCGAAA	660	
CACTTACTGA	AGACGAATAG	CTATGGGAAG	AACAGGATAA	CCCGTGACCA	AGTTAAGAAG	720	
ATAATTATGG	CAATTGTGCT	TTTCTTTTC	TTTCCTGG	TTCCCCACCA	AATATTCACT	780	
25 TTTCTGGATG	TATTGATTCA	ACTAGGCATC	ATACGTGACT	GTAGAATTGC	AGATATTGTG	840	
GACACGGCCA	TGCCTATCAC	CATTTGTATA	GCTTATTTA	ACAATTGCCT	GAATCCTCTT	900	
TTTTATGGCT	TTCTGGGAA	AAAATTAAA	AGATATTTTC	TCCAGCTTCT	AAAATATATT	960	
CCCCCAAAAG	CCAAATCCC	CTCAACCTT	TCAACAAAAA	TGAGCACGCT	TTCCTACCGC	1020	
CCCTCAGATA	ATGTAAGCTC	ATCCACCAAG	AAGCCTGCAC	CATGTTTGA	GGTTGAGTGA	1080	

(101) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
5 (C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
10 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35 35 40 45

15 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
50 55 60

Val Phe Leu Leu Asn Leu Ala Asp Leu Cys Phe Leu Leu Thr
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
20 85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
115 120 125

25 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
130 135 140

Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
30 165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
195 200 205

35 Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys
210 215 220

Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His
245 250 255

5 Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
275 280 285

10 Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
325 330 335

15 Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
340 345 350

Ala Pro Cys Phe Glu Val Glu
355

(102) INFORMATION FOR SEQ ID NO:101:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCCGAATTCC AAAATAACTT GTAAGAATGA TCAGAAA

37

(103) INFORMATION FOR SEQ ID NO:102:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGATCTTAAG AAGATAATTA TGGCAATTGT GCT

33

(104) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AATTCGAAAA CACTTACTGA AGACGAATAG CTATGGGAAG AACAGGATAA CCCGTGACCA

60

AG

62

(105) INFORMATION FOR SEQ ID NO:104:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTAACTTGGT CACGGGTTAT CCTGTTCTTC CCATAGCTAT TCGTCTTCAG TAAGTGTTT

60

CG

62

25 (106) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCAAA 60
 GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCTACTT TATACAGTAT CATCTTGTG 120
 GTGGGAATAT TTGGAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG 180
 ACTGTGGCCA GTGTTTTCT TTTGAATTAA CACACTGGCTG ACTTATGCTT TTTACTGACT 240
 5 TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA 300
 TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCACG 360
 TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC 420
 ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGCCAGT 480
 TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTGT 540
 10 GCTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAT 600
 ATAATGGGTT TCCTGTTCC TTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG 660
 GCCCTAAAGA AGGCTTATGA AATTAGAAG AACAAACCAA GAAATGATGA TATTTTTAAG 720
 ATAATTATGG CAGCAATTGT GCTTTCTTT TTCTTTCCCT GGATTCCCCA CCAAATATTC 780
 ACTTTCTGG ATGTATTGAT TCAACTAGGC ATCATACTGT ACTGTAGAAT TGCAGATATT 840
 15 GTGGACACGG CCATGCCTAT CACCATTGT ATAGCTTATT TTAACAATTG CCTGAATCCT 900
 CTTTTTATG GCTTCTGGG GAAAAAATT AAAAGATATT TTCTCCAGCT TCTAAAATAT 960
 ATTCCCCAA AAGCCAAATC CCACTCAAAC CTTCAACAA AAATGAGCAC GCTTCCCTAC 1020
 CGCCCCTCAG ATAATGTAAG CTCATCCACC AAGAAGCCTG CACCATGTT TGAGGTTGAG 1080
 TGA 1083

20 (107) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

25 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
 1 5 10 15

30 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro

	20	25	30
	Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu		
	35	40	45
5	Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser		
	50	55	60
	Val Phe Leu Leu Asn Leu Ala Asp Leu Cys Phe Leu Leu Thr		
	65	70	75
	80		
	Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe		
	85	90	95
10	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu		
	100	105	110
	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
15	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155
	160		
	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
20	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
25	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
	225	230	235
	240		
	Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro		
	245	250	255
30	His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile		
	260	265	270
	Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr		
	275	280	285
	Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly		
35	290	295	300
	Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr		
	305	310	315
	320		

Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser
325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys
340 345 350

5 Pro Ala Pro Cys Phe Glu Val Glu
355 360

(108) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(109) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AAGCACAAATT GCTGCATAAT TATCTAAAAA ATATCATC

38

(110) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAGATAATTA TGGCAGCAAT TGTGCTTTTC TTTTTCTTT

39

(111) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGATCCA CATAATGCAT TTTCTC

26

(112) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGGAGCTGC	TAAAGCTGAA	CCGGAGCGTG	CAGGGAACCG	GACCCGGGCC	GGGGGCTTCC	60
CTGTGCCGCC	CGGGGGCGCC	TCTCCTCAAC	AGCAGCAGTG	TGGGCAACCT	CAGCTGCGAG	120
CCCCCTCGCA	TTCGCGGAGC	CGGGACACGA	GAATTGGAGC	TGGCCATTAG	AATCACTCTT	180
TACGCAGTGA	TCTTCCTGAT	GAGCGTTGGA	GGAAATATGC	TCATCATCGT	GGTCCTGGGA	240
25 CTGAGCCGCC	GCCTGAGGAC	TGTCACCAAT	GCCTTCCTCC	TCTCACTGGC	AGTCAGCGAC	300
CTCCTGCTGG	CTGTGGCTTG	CATGCCCTTC	ACCCTCCTGC	CCAATCTCAT	GGGCACATTC	360
ATCTTTGGCA	CCGTCATCTG	CAAGGCAGTT	TCCTACCTCA	TGGGGGTGTC	TGTGAGTGTG	420
TCCACGCTAA	GCCTCGTGGC	CATCGCACTG	GAGCGATATA	GCGCCATCTG	CCGACCACTG	480
CAGGCACGAG	TGTGGCAGAC	GCGCTCCAC	GCGGCTCGCG	TGATTGTAGC	CACGTGGCTG	540
30 CTGTCCGGAC	TACTCATGGT	GCCCTACCCC	GTGTACACTG	TCGTGCAACC	AGTGGGGCCT	600
CGTGTGCTGC	AGTGGCGTGCA	TCGCTGGCCC	AGTGGCGGGG	TCCGCCAGAC	CTGGTCCGTA	660

CTGCTGCTTC	TGCTCTTGT	TTTCATCCCA	GGTGTGGTTA	TGGCCGTGGC	CTACGGGCTT	720	
ATCTCTCGCG	AGCTCTACTT	AGGGCTTCGC	TTTGACGGCG	ACAGTGACAG	CGACAGCCAA	780	
AGCAGGGTCC	GAAACCAAGG	CGGGCTGCCA	GGGGCTGTT	ACCAGAACGG	GCGTTGCCGG	840	
CCTGAGACTG	GCGCGGTTGG	CAAAGACAGC	GATGGCTGCT	ACGTGCAACT	TCCACGTTCC	900	
5	CGGCCTGCC	TGGAGCTGAC	GGCGCTGACG	GCTCCTGGC	CGGGATCCGG	CTCCCGGCC	960
	ACCCAGGCCA	AGCTGCTGGC	TAAGAAGCGC	GTGAAACGAA	TGTTGCTGGT	GATCGTTGTG	1020
	CTTTTTTTTC	TGTGTTGGTT	GCCAGTTTAT	AGTGCCAACA	CGTGGCGCGC	CTTGATGGC	1080
	CCGGGTGCAC	ACCGAGCACT	CTCGGGTGCT	CCTATCTCCT	TCATTCACTT	GCTGAGCTAC	1140
	GCCTCGGCCT	GTGTCAACCC	CCTGGTCTAC	TGCTTCATGC	ACCGTCGCTT	TCGCCAGGCC	1200
10	TGCCTGGAAA	CTTGCCTCG	CTGCTGCC	CGGCCTCCAC	GAGCTGCC	CAGGGCTCTT	1260
	CCCGATGAGG	ACCCTCCCAC	TCCCTCCATT	GCTTCGCTGT	CCAGGCTTAG	CTACACCACC	1320
	ATCAGCACAC	TGGGCCCTGG	CTGA				1344

(113) INFORMATION FOR SEQ ID NO:112:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

25 Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

30 Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95

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Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
115 120 125

5 Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Thr Leu Ser
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145 150 155 160

10 Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
195 200 205

15 Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
225 230 235 240

20 Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys
275 280 285

25 Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
305 310 315 320

30 Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu
325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
355 360 365

35 Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala

385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
405 410 415

5 Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
435 440 445

(114) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CAGCAGCATG CGCTTCACGC GCTTCTTAGC CCAG

34

(115) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

25 AGAAGCGCGT GAAGCGCATG CTGCTGGTGA TCGTT

35

(116) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

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ATGGAGAAAA GAATCAAAAG AATGTTCTAT ATA

33

(117) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TATATAGAAC ATTCTTTGATTCCTTTCTCAT

33

(118) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGCTCTCTGG CCTTGAAGCGCACGCTCAGC

30

(119) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCTGAGCGTG CGCTTCAAGGCCAGAGAGCG

30

(120) INFORMATION FOR SEQ ID NO:119:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCAGGAAAAA AGGTGAAAGT CAAAGTTTTC

30

10 (121) INFORMATION FOR SEQ ID NO:120:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAAAACTTTG ACTTTCACCT TTTTCCTGGG

30

20 (122) INFORMATION FOR SEQ ID NO:121:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGGGCGCGGG TGAAACGGCT GGTGAGC

27

30 (123) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

5 GCTCACCAAGC CGTTTCACCC GCGCCCC

27

(124) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

15 CCCCTTGAAA AGCCTAAGAA CTTGGTCATC

30

(125) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

25 GATGACCAAG TTCTTAGGCT TTTCAAGGGG

30

(126) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATCTCTAGA ATGAACAGCA CATGTATTGA AG

32

(127) INFORMATION FOR SEQ ID NO:126:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTAGGGTACC CGCTCAAGGA CCTCTAATTC CATAG

35

(128) INFORMATION FOR SEQ ID NO:127:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGCAGGCAG TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAAACCTG

60

ACGCAGGGAGC AGTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG

120

CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC

180

25 TTTGGCAATG CTCTGGTGTG CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC

240

AACATCTTA TCTGCTCCTT GGCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC

300

GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGG GTGCTTCAT TTGCAAGATG

360

GTGCCATTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT

420

GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA

480

AGGGCTTC	CAATGCTAGG	TGTGGTCTGG	CTGGTGGCAG	TCATCGTAGG	ATCACCCATG	540
TGGCACGTGC	AACAAC TTGA	GATCAAATAT	GACTTCCTAT	ATGAAAAGGA	ACACATCTGC	600
TGCTTAGAAG	AGTGGACCAG	CCCTGTGCAC	CAGAAGATCT	ACACCACCTT	CATCCTTGTC	660
ATCCTCTTCC	TCCTGCCTCT	TATGGTGATG	CTTATTCTGT	ACAGTAAAAT	TGGTTATGAA	720
5 CTTTGGATAA	AGAAAAGAGT	TGGGGATGGT	TCAGTGCTTC	GAACATTCA	TGGAAAAGAA	780
ATGTCCAAAA	TAGCCAGGAA	GAAGAAACGA	GCTAAGATTA	TGATGGTGAC	AGTGGTGGCT	840
CTCTTGCTG	TGTGCTGGC	ACCATTCCAT	GTTGTCCATA	TGATGATTGA	ATACAGTAAT	900
TTTGAAAAGG	AATATGATGA	TGTCACAATC	AAGATGATT	TTGCTATCGT	GCAAATTATT	960
GGATTTCCA	ACTCCATCTG	TAATCCCATT	GTCTATGCAT	TTATGAATGA	AAACTTCAAA	1020
10 AAAAATGTTT	TGTCTGCAGT	TTGTTATTGC	ATAGTAAATA	AAACCTTCTC	TCCAGCACAA	1080
AGGCATGGAA	ATTCAGGAAT	TACAATGATG	CGGAAGAAAG	CAAAGTTTC	CCTCAGAGAG	1140
AATCCAGTGG	AGGAAACCAA	AGGAGAAGCA	TTCAGTGATG	GCAACATTGA	AGTCAAATTG	1200
TGTGAACAGA	CAGAGGAGAA	GAAAAAGCTC	AAACGACATC	TTGCTCTTT	TAGGTCTGAA	1260
CTGGCTGAGA	ATTCTCCTTT	AGACAGTGGG	CATTAA			1296
15 (128) INFORMATION FOR SEQ ID NO:128:						

15 (129) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

	Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe			
	85	90	95	
	Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu			
	100	105	110	
5	Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala			
	115	120	125	
	Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His			
	130	135	140	
10	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg			
	145	150	155	160
	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val			
	165	170	175	
	Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe			
	180	185	190	
15	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro			
	195	200	205	
	Val His Gln Lys Ile Tyr Thr Phe Ile Leu Val Ile Leu Phe Leu			
	210	215	220	
20	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu			
	225	230	235	240
	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile			
	245	250	255	
	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Arg Ala Lys			
	260	265	270	
25	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro			
	275	280	285	
	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu			
	290	295	300	
30	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile			
	305	310	315	320
	Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn			
	325	330	335	
	Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val			
	340	345	350	
35	Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr			
	355	360	365	
	Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu			

370

375

380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
385 390 395 400

5 Cys Glu Gln Thr Glu Glu Lys Lys Leu Lys Arg His Leu Ala Leu
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
420 425 430

(130) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 2040 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGGGCAGCC CCTGGAACGG CAGCGACGGC CCCGAGGGGG CGCGGGAGCC GCCGTGGCCC
60

GCGCTGCCGC CTTGCGACGA GCGCCGCTGC TCGCCCTTTC CCCTGGGGGC GCTGGTGCCG
120

20 GTGACCGCTG TGTGCCTGTG CCTGTTCGTC GTCGGGGTGA GCGGCAACGT GGTGACCGTG
180

ATGCTGATCG GGCGCTACCG GGACATGCGG ACCACCACCA ACTTGTACCT GGGCAGCATG
240

25 GCCGTGTCCG ACCTACTCAT CCTGCTCGGG CTGCCGTTCG ACCTGTACCG CCTCTGGCCG
300

TCGCGGCCCT GGGTGTTCGG GCCGCTGCTC TGCCGCCTGT CCCTCTACGT GGGCGAGGGC
360

30 TGCACCTACG CCACGCTGCT GCACATGACC GCGCTCAGCG TCGAGCGCTA CCTGGCCATC
420

TGCCGCCCGC TCCGCGCCCG CGTCTTGGTC ACCCGGCGCC GCGTCCGCGC GCTCATCGCT
480

35 GTGCTCTGGG CCGTGGCGCT GCTCTCTGCC GGTCCCTTCT TGTTCCCTGGT GGGCGTCGAG
540

CAGGACCCCG GCATCTCCGT AGTCCCGGGC CTCAATGGCA CCGCGCGGAT CGCCTCCTCG
600

40 CCTCTCGCCT CGTCGCCGCC TCTCTGGCTC TCGCGGGCGC CACCGCCGTC CCCGCCGTCG

660
GGGCCGAGA CCGCGGAGGC CGCGCGCTG TTCAGCCGCG AATGCCGCC GAGCCCCGCG
720
5 CAGCTGGCG CGCTGCGTGT CATGCTGTGG GTCACCACCG CCTACTTCTT CCTGCCCTT
780
CTGTGCCTCA GCATCCTCTA CGGGCTCATC GGGCGGGAGC TGTGGAGCAG CGGGCGGCCG
10 840
CTGCGAGGCC CGGCCGCCTC GGGGCGGGAG AGAGGCCACC GGCAGACCAA ACGCGTCCTG
900
15 CGTAAGTGGA GCCGCCGTGG TTCCAAAGAC GCCTGCCTGC AGTCCGCCCC GCCGGGGACC
960
GCGCAAACGC TGGGTCCCCT TCCCCGTCT GCCTGCCTGC TCCAGCTCCC
1020
20 TTTCTATTT CGATTCCAGC CTCCACCCGC CGGTACTTCC CATCCCCGA GAAAACCATG
1080
TCCTGTCCCC CAGGAGCTCT GGGGACCCC AGGGCGCTTT GAGGGTGGGA TCCCCGGATC
25 1140
CGATTCAAGTA ACCAGCAGTG CTTTCCAGA GCCTCTGAGA CCAGAAAGGA GAGTTGGTAA
1200
30 TTCTTAATCC AACACACCTGT TAGATGCCAC AAATGAGGAG TCCTCACAGT GCTCTTGAGA
1260
AGACGAGGGA GATTTCATTA AGCTAAAATT TTTTATTTAA TGTTAAGTGA TGCTGAAGGC
1320
35 TAAAGTAAAC CTTGCTCGTA TCAAAAAGTA AAGATTGTGC AGACCTGTTG TAGAATTCTT
1380
TTCAACAGAG AACAGAAAAC TTGTCTCCGA AGTGGGTTTG TGGAAGGAAG CCTGCCAAGG
40 1440
CGGCTTGTTC AGAGAAATTG CTCCTCTGG TTTATGTCCA GCCTTGATAA CACATATGGG
1500
45 AGCCTACTAT GCAGTTTAA AGCAAGTATC CATGCAGCCT GCAGCCTGGT CATTTCCTCT
1560
GGGGTGAGGA TCTGCCTAGG TAGAAGTTTT CTCTAATTAA TTTTGCTGTT ACTTGTTATT
1620
50 GCAGATGGTT CCTTGTCGGG GTGGGGGGTT TATTTGCTTC CCAATGCTTT TGTTAATCCC
1680
55 GGTGCTGTGT CTTATGTTGC AGTGGTGGTG GTTCTGGCAT TTATAATTG CTGGTTGCC
1740

TTCCACGTTG GCAGAACAT TTACATAAAC ACGGAAGATT CGCGGATGAT GTACTTCTCT
1800

5 CAGTACTTTA ACATCGTCGC TCTGCAACTT TTCTATCTGA GCGCATCTAT CAACCCAATC
1860

CTCTACAACC TCATTTCAAA GAAAGTACAGA GCGGCGGCCT TTAAACTGCT GCTCGCAAGG
1920

10 AAGTCCAGGC CGAGAGGCTT CCACAGAACG AGGGACACTG CGGGGAAAGT TGCAGGGAC
1980

ACTGGAGGAG ACACGGTGGG CTACACCGAG ACAAGCGCTA ACGTGAAGAC GATGGGATAA
15 2040

(131) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids
20 (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

25 Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu
1 5 10 15

Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
20 25 30

Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
35 40 45

30 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
50 55 60

Arg Tyr Arg Asp Met Arg Thr Thr Asn Leu Tyr Leu Gly Ser Met
65 70 75 80

35 Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr
85 90 95

Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg
100 105 110

Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His
115 120 125

40 Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
130 135 140

Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala
145 150 155 160

Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu
165 170 175

5 Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn
180 185 190

Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu
195 200 205

10 Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr
210 215 220

Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala
225 230 235 240

Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe
245 250 255

15 Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg
260 265 270

Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly
275 280 285

20 Arg Glu Arg Gly His Arg Gln Thr Lys Arg Val Leu Leu Val Val Val
290 295 300

Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile
305 310 315 320

Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe
325 330 335

25 Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro
340 345 350

Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Phe Lys
355 360 365

30 Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg
370 375 380

Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly
385 390 395 400

Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly
405 410

35 (132) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1344 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGAGCTGC TAAAGCTGAA CGGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC
60
CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG
120
10 CCCCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT
180
TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTGGGA
240
CTGAGCCGCC GCCTGAGGAC TGTCACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC
15 300
CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTG
360
ATCTTTGGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG
420
20 TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACGT
480
CAGGCACGAG TGTGGCAGAC GCGCTCCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG
540
CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT
25 600
CGTGTGCTGC AGTGCCTGCA TCGCTGGCCC AGTGCCTGGG TCCGCCAGAC CTGGTCCGTA
660
CTGCTGCTTC TGCTCTTGTGTT CTTCATCCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT
720
30 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTTGACGGCG ACAGTGACAG CGACAGCCAA
780
AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTA ACCAGAACGG GCGTTGCCGG
840
CCTGAGACTG GCGCGGTTGG CAAAGACAGC GATGGCTGCT ACGTGCAACT TCCACGTTCC
35 900
CGGCCTGCCCG TGGAGCTGAC GGCGCTGACG GCTCCTGGGC CGGGATCCGG CTCCCGGCC

960

ACCCAGGCCA AGCTGCTGGC TAAGAAGCGC GTGAAACGAA TGTTGCTGGT GATCGTTGTG
1020

5 CTTTTTTTTC TGTGTTGGTT GCCAGTTTAT AGTGCCAACA CGTGGCGCGC CTTTGATGGC
1080

CGGGGTGCAC ACCGAGCACT CTCGGGTGCT CCTATCTCCT TCATTCACCT GCTGAGCTAC
1140

GCCCTGGCCT GTGTCAACCC CCTGGTCTAC TGCTTCATGC ACCGTCGCTT TCGCCAGGCC
1200

10 TGCCTGGAAA CTTGCGCTCG CTGCTGCCCC CGGCCTCCAC GAGCTGCC CAGGGCTCTT
1260

CCCGATGAGG ACCCTCCAC TCCCTCCATT GCTTCGCTGT CCAGGCTTAG CTACACCACC
1320

ATCAGCACAC TGGGCCCTGG CTGA

15 1344

(133) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
20 (C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

25 Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

30 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

35 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu

	100	105	110
	Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys		
	115	120	125
5	Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser		
	130	135	140
	Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu		
	145	150	155
	Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val		
	165	170	175
10	Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr		
	180	185	190
	Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg		
	195	200	205
15	Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu		
	210	215	220
	Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu		
	225	230	235
	Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp		
	245	250	255
20	Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala		
	260	265	270
	Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys		
	275	280	285
25	Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu		
	290	295	300
	Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro		
	305	310	315
	Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu		
	325	330	335
30	Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala		
	340	345	350
	Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser		
	355	360	365
35	Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys		
	370	375	380
	Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala		
	385	390	395

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
 405 410 415
 Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
 420 425 430
 5 Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
 435 440 445

(134) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

15	ATGAACAGCA CATGTATTGA AGAACAGCAT GACCTGGATC ACTATTTGTT TCCCATTGTT	60
	TACATCTTG TGATTATAGT CAGCATTCCA GCCAATATTG GATCTCTGTG TGTGTCTTC	120
	CTGCAAGCAA AGAAGGAAAG TGAACCTAGGA ATTTACCTCT TCAGTTGTC ACTATCAGAT	180
	TTACTCTATG CATTAACTCT CCCTTTATGG ATTGATTATA CTTGGAATAA AGACAACTGG	240
	ACTTTCTCTC CTGCCTTGTG CAAAGGGAGT GCTTTCTCA TGTACATGAA TTTTACAGC	300
20	AGCACAGCAT TCCTCACCTG CATTGCCGTT GATCGGTATT TGGCTGTTGT CTACCCTTG	360
	AAGTTTTTT TCCTAAGGAC AAGAAGATT GCACTCATGG TCAGCCTGTC CATCTGGATA	420
	TTGGAAACCA TCTTCAATGC TGTCTGTTG TGGGAAGATG AAACAGTTGT TGAATATTGC	480
	GATGCCGAAA AGTCTAATTT TACTTTATGC TATGACAAAT ACCCTTACA GAAATGGCAA	540
	ATCAACCTCA ACTTGTTCAG GACGTGTACA GGCTATGCAA TACCTTGGT CACCATCCTG	600
25	ATCTGTAACC GGAAAGTCTA CCAAGCTGTG CGGCACAATA AAGCCACGGA AAACAAGGAA	660
	AAGAAGAGAA TCAAAAAACT ACTTGTCAAGC ATCACAGTTA CTTTGTCTT ATGCTTTACT	720
	CCCTTTCATG TGATGTTGCT GATTGCTGC ATTTAGAGC ATGCTGTGAA CTTCGAAGAC	780
	CACAGCAATT CTGGGAAGCG AACTTACACA ATGTATAGAA TCACGGTTGC ATTAACAAGT	840
	TTAAATTGTG TTGCTGATCC AATTCTGTAC TGTTTGTAA CCGAAACAGG AAGATATGAT	900
30	ATGTGGAATA TATTAATT CTGCACTGGG AGGTGTAATA CATCACAAAG ACAAAAGAAAA	960
	CGCATACTTT CTGTGTCTAC AAAAGATACT ATGGAATTAG AGGTCTTGA GTAG	1014

(135) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 amino acids
(B) TYPE: amino acid
5 (C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

10	Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu 1 5 10 15
15	Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn 20 25 30
20	Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu Ser Glu 35 40 45
25	Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala 50 55 60
30	Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp 65 70 75 80
35	Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met 85 90 95
40	Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg 100 105 110
45	Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg 115 120 125
50	Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile 130 135 140
55	Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys 145 150 155 160
60	Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu 165 170 175
65	Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr 180 185 190
70	Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln 195 200 205
75	Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile 210 215 220

Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
245 250 255

5 Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
275 280 285

10 Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
325 330 335

15 Glu

(136) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

25 ATGGTGAACCT CCACCCACCG TGGGATGCAC ACTTCTCTGC ACCTCTGGAA CCGCAGCAGT
60

TACAGACTGC ACAGCAATGC CAGTGAGTCC CTTGGAAAAG GCTACTCTGA TGGAGGGTGC
120

TACGAGCAAC TTTTGTCCTC TCCTGAGGTG TTTGTGACTC TGGGTGTCAT CAGCTTGTG
30 180

GAGAATATCT TAGTGATTGT GGCAATAGCC AAGAACAAAGA ATCTGCATTC ACCCATGTAC
240

TTTTTCATCT GCAGCTTGGC TGTGGCTGAT ATGCTGGTGA GCGTTCAAA TGGATCAGAA
300

35 ACCATTATCA TCACCCATTAAACAGTACA GATAACGGATG CACAGAGTTT CACAGTGAAT
360

ATTGATAATG TCATTGACTC GGTGATCTGT AGCTCCTTGC TTGCATCCAT TTGCAGCCTG
420

CTTTCAATTG CAGTGGACAG GTACTTTACT ATCTTCTATG CTCTCCAGTA CCATAACATT
480

5 ATGACAGTTA AGCGGGTTGG GATCAGCATA AGTTGTATCT GGGCAGCTTG CACGGTTCA
540

GGCATTGT TCATCATTAA CTCAGATAGT AGTGCTGTCA TCATCTGCCT CATCACCATG
600

10 TTCTTCACCA TGCTGGCTCT CATGGCTTCT CTCTATGTCC ACATGTTCCCT GATGGCCAGG
660

CTTCACATTA AGAGGATTGC TGTCCCTCCCC GGCACGGTG CCATCCGCCA AGGTGCCAAT
720

ATGAAGGGAA AAATTACCTT GACCATCCTG ATTGGCGTCT TTGTTGTCTG CTGGGCCCA
780

15 TTCTTCCTCC ACTTAATATT CTACATCTCT TGTCCCTCAGA ATCCATATTG TGTGTGCTTC
840

ATGTCTCACT TTAACCTGTA TCTCATACTG ATCATGTGTA ATTCAATCAT CGATCCTCTG
900

20 ATTTATGCAC TCCGGAGTCA AGAACTGAGG AAAACCTTCA AAGAGATCAT CTGTTGCTAT
960

CCCCCTGGGAG GCCTTTGTGA CTTGTCTAGC AGATATTAA
999

(137) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
20 25 30

35 Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro
35 36 37 38 39 40 41 42 43 44 45

	Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu	
	50 55 60	
	Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr	
	65 70 75 80	
5	Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser	
	85 90 95	
	Asn Gly Ser Glu Thr Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr	
	100 105 110	
10	Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val	
	115 120 125	
	Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala	
	130 135 140	
	Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile	
	145 150 155 160	
15	Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala	
	165 170 175	
	Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala	
	180 185 190	
20	Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met	
	195 200 205	
	Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys	
	210 215 220	
	Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn	
	225 230 235 240	
25	Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val	
	245 250 255	
	Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro	
	260 265 270	
30	Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu	
	275 280 285	
	Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu	
	290 295 300	
	Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr	
	305 310 315 320	
35	Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr	
	325 330	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCAATATGA AGGGAAAAAT TACCTTGACC ATC
33

10 (137) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T
31

20 (140) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGGGGCCCA CCCTAGCGGT TCCCACCCCC TATGGCTGTA TTGGCTGTAA GCTACCCAG	60
CCAGAAATACC CACCGGCTCT AATCATCTT ATGTTCTGCG CGATGGTTAT CACCATCGTT	120
30 GTAGACCTAA TCGGCAACTC CATGGTCATT TTGGCTGTGA CGAAGAACAA GAAGCTCCGG	180
AATTCTGGCA ACATCTTCGT GGTCAGTCTC TCTGTGGCCG ATATGCTGGT GGCCATCTAC	240
CCATACCCCTT TGATGCTGCA TGCCATGTCC ATTGGGGCT GGGATCTGAG CCAGTTACAG	300
TGCCAGATGG TCGGGTTCAT CACAGGGCTG AGTGTGGTCG GCTCCATCTT CAACATCGTG	360

GCAATCGCTA	TCAACCGTTA	CTGCTACATC	TGCCACAGCC	TCCAGTACGA	ACGGATCTTC	420	
AGTGTGCGCA	ATACCTGCAT	CTACCTGGTC	ATCACCTGGA	TCATGACCGT	CCTGGCTGTC	480	
CTGCCAACA	TGTACATTGG	CACCATCGAG	TACGATCCTC	GCACCTACAC	CTGCATCTTC	540	
AACTATCTGA	ACAACCCTGT	CTTCACTGTT	ACCATCGTCT	GCATCCACTT	CGTCCTCCCT	600	
5	CTCCTCATCG	TGGTTTCTG	CTACGTGAGG	ATCTGGACCA	AAGTGTGGC	GGCCCGTGAC	660
CCTGCAGGGC	AGAATCCTGA	CAACCAAATT	GCTGAGGTTTC	GCAATTTCT	AACCATGTTT	720	
GTGATCTTCC	TCCTCTTGC	AGTGTGCTGG	TGCCCTATCA	ACGTGCTCAC	TGTCTGGTG	780	
GCTGTCAGTC	CGAAGGAGAT	GGCAGGCAAG	ATCCCCAACT	GGCTTATCT	TGCAGCCTAC	840	
TTCATAGCCT	ACTTCAACAG	CTGCCTCAAC	GCTGTGATCT	ACGGGCTCCT	CAATGAGAAT	900	
10	TTCCGAAGAG	AATACTGGAC	CATCTCCAT	GCTATGCGGC	ACCCTATCAT	ATTCTCCCT	960
GGCCTCATCA	GTGATATTG	TGAGATGCAG	GAGGCCCGTA	CCCTGGCCCG	CGCCCGTGCC	1020	
CATGCTCGCG	ACCAAGCTCG	TGAACAAGAC	CGTGCCCATG	CCTGTCCTGC	TGTGGAGGAA	1080	
ACCCCGATGA	ATGTCCGGAA	TGTTCCATTA	CCTGGTGATG	CTGCAGCTGG	CCACCCCGAC	1140	
CGTGCCTCTG	GCCACCCCTAA	GCCCCATTCC	AGATCCTCCT	CTGCCTATCG	CAAATCTGCC	1200	
15	TCTACCCACC	ACAAGTCTGT	CTTTAGCCAC	TCCAAGGCTG	CCTCTGGTCA	CCTCAAGCCT	1260
GTCTCTGGCC	ACTCCAAGCC	TGCCTCTGGT	CACCCCAAGT	CTGCCACTGT	CTACCCTAAG	1320	
CCTGCCTCTG	TCCATTCAA	GGGTGACTCT	GTCCATTCA	AGGGTGACTC	TGTCCATTTC	1380	
AAGCCTGACT	CTGTTCATTT	CAAGCCTGCT	TCCAGCAACC	CCAAGCCCAT	CACTGGCCAC	1440	
CATGTCTCTG	CTGGCAGCCA	CTCCAAGTCT	GCCTTCAGTG	CTGCCACCAG	CCACCCCTAAA	1500	
20	CCCATCAAGC	CAGCTACCAAG	CCATGCTGAG	CCCACCACTG	CTGACTATCC	CAAGCCTGCC	1560
ACTACCAGCC	ACCTTAAGCC	CGCTGCTGCT	GACAACCTG	AGCTCTCTGC	CTCCCATTGC	1620	
CCCGAGATCC	CTGCCATTGC	CCACCCGTG	TCTGACGACA	GTGACCTCCC	TGAGTCGGCC	1680	
TCTAGCCCTG	CCGCTGGGCC	CACCAAGCCT	GCTGCCAGCC	AGCTGGAGTC	TGACACCATC	1740	
GCTGACCTTC	CTGACCCCTAC	TGTAGTCACT	ACCAGTACCA	ATGATTACCA	TGATGTCGTG	1800	
25	GTTGTTGATG	TTGAAGATGA	TCCTGATGAA	ATGGCTGTGT	GA	1842	

(141) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

5 Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
1 5 10 15

Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
20 25 30

Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
10 35 40 45

Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
65 70 75 80

15 Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
 85 90 95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
100 105 110

Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
20 115 120 125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
145 150 155 160

25 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
 165 170 175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
180 185 190

Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
30 195 200 205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
210 215 220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe
225 230 235 240

35 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
 245 250 255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
260 265 270

Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
275 280 285

5 Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
290 295 300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro
305 310 315 320

Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala
10 325 330 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala
340 345 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val
355 360 365

15 Pro Leu Pro Gly Asp Ala Ala Gly His Pro Asp Arg Ala Ser Gly
370 375 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala
385 390 395 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly
20 405 410 415

His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro
420 425 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly
435 440 445

25 Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser
450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His
465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr
30 485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr
500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala
515 520 525

35 Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro
530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala

10 (142) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ATGGGGCCCA	CCCTAGCGGT	TCCCACCCCC	TATGGCTGTA	TTGGCTGTAA	GCTACCCCCAG	60	
CCAGAAATACC	CACCGGCTCT	AATCATCTT	ATGTTCTGCG	CGATGGTTAT	CACCATCGTT	120	
20	GTAGACCTAA	TCGGCAACTC	CATGGTCATT	TTGGCTGTGA	CGAAGAACAA	GAAGCTCCGG	180
	AATTCTGGCA	ACATCTTCGT	GGTCAGTCTC	TCTGTGGCCG	ATATGCTGGT	GGCCATCTAC	240
	CCATACCCCTT	TGATGCTGCA	TGCCATGTCC	ATTGGGGGCT	GGGATCTGAG	CCAGTTACAG	300
	TGCCAGATGG	TCGGGTTCAT	CACAGGGCTG	AGTGTGGTCG	GCTCCATCTT	CAACATCGTG	360
	GCAATCGCTA	TCAACCGTTA	CTGCTACATC	TGCCACAGCC	TCCAGTACGA	ACGGATCTTC	420
25	AGTGTGCGCA	ATACCTGCAT	CTACCTGGTC	ATCACCTGGA	TCATGACCGT	CCTGGCTGTC	480
	CTGCCCAACA	TGTACATTGG	CACCATCGAG	TACGATCCTC	GCACCTACAC	CTGCATCTTC	540
	AACTATCTGA	ACAACCCCTGT	CTTCACTGTT	ACCATCGTCT	GCATCCACTT	CGTCCTCCCT	600
	CTCCTCATCG	TGGGTTTCTG	CTACGTGAGG	ATCTGGACCA	AAGTGCTGGC	GGCCCGTGAC	660
	CCTGCAGGGC	AGAATCCTGA	CAACCAACTT	GCTGAGGTTTC	GCAATAAACT	AACCATGTTT	720
30	GTGATCTTCC	TCCTCTTGC	AGTGTGCTGG	TGCCCTATCA	ACGTGCTCAC	TGTCTTGGTG	780
	GCTGTCAGTC	CGAAGGGAGAT	GGCAGGCAAG	ATCCCCAACT	GGCTTTATCT	TGCAGCCTAC	840

	TTCATAGCCT	ACTTAACAG	CTGCCTAAC	GCTGTGATCT	ACGGGCTCCT	CAATGAGAAT	900
	TTCCGAAGAG	AATACTGGAC	CATCTTCCAT	GCTATGCGGC	ACCCTATCAT	ATTCTTCTCT	960
	GGCCTCATCA	GTGATATTG	TGAGATGCAG	GAGGCCCGTA	CCCTGGCCCG	CGCCCGTGCC	1020
	CATGCTCGCG	ACCAAGCTCG	TGAACAAGAC	CGTGCCCATG	CCTGTCCTGC	TGTGGAGGAA	1080
5	ACCCCGATGA	ATGTCCGGAA	TGTTCCATT	CCTGGTGATG	CTGCAGCTGG	CCACCCCGAC	1140
	CGTGCCTCTG	GCCACCCCTAA	GCCCCATTCC	AGATCCTCCT	CTGCCTATCG	CAAATCTGCC	1200
	TCTACCCACC	ACAAGTCTGT	CTTTAGCCAC	TCCAAGGCTG	CCTCTGGTCA	CCTCAAGCCT	1260
	GTCTCTGGCC	ACTCCAAGCC	TGCCTCTGGT	CACCCCAAGT	CTGCCACTGT	CTACCCCTAAG	1320
	CCTGCCTCTG	TCCATTCAA	GGCTGACTCT	GTCCATTCA	AGGGTGACTC	TGTCCATTTC	1380
10	AAGCCTGACT	CTGTTCATTT	CAAGCCTGCT	TCCAGCAACC	CCAAGCCCAT	CACTGGCCAC	1440
	CATGTCTCTG	CTGGCAGCCA	CTCCAAGTCT	GCCTTCAATG	CTGCCACCAG	CCACCCCTAAA	1500
	CCCATCAAGC	CAGCTACCAAG	CCATGCTGAG	CCCACCACTG	CTGACTATCC	CAAGCCTGCC	1560
	ACTACCAGCC	ACCCCTAAGCC	CGCTGCTGCT	GACAACCCTG	AGCTCTCTGC	CTCCCATTGC	1620
	CCCGAGATCC	CTGCCATTGC	CCACCCCTGTG	TCTGACGACA	GTGACCTCCC	TGAGTCGGCC	1680
15	TCTAGCCCTG	CCGCTGGGCC	CACCAAGCCT	GCTGCCAGCC	AGCTGGAGTC	TGACACCATC	1740
	GCTGACCTTC	CTGACCCCTAC	TGTAGTCACT	ACCAGTACCA	ATGATTACCA	TGATGTCGTG	1800
	GTTGTTGATG	TTGAAGATGA	TCCTGATGAA	ATGGCTGTGT	GA		1842

(143) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 613 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
1           5           10          15

Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
20          25          30

Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
35          40          45

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Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
65 70 75 80

5 Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
85 90 95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
100 105 110

10 Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
115 120 125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val
145 150 155 160

15 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr
165 170 175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile
180 185 190

20 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr
195 200 205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln
210 215 220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Lys Leu Thr Met Phe
225 230 235 240

25 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu
245 250 255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro
260 265 270

30 Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys
275 280 285

Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu
290 295 300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Ser
305 310 315 320

35 Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala
325 330 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala

340 345 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val
355 360 365

5 Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly
370 375 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala
385 390 395 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly
405 410 415

10 His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro
420 425 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala
435 440 445

15 Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser
450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His
465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr
485 490 495

20 Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr
500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala
515 520 525

25 Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro
530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala
545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu
565 570 575

30 Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser
580 585 590

Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro
595 600 605

35 Asp Glu Met Ala Val
610

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GCTGAGGTTC GCAATAAACT AACCATGTTT GTG

33

(145) INFORMATION FOR SEQ ID NO:144:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(146) INFORMATION FOR SEQ ID NO:145:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTAGATATCG GGGCCCACCC TAGCGGT

33

(147) INFORMATION FOR SEQ ID NO:146:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGTACCCCA CAGCCATTTC ATCAGGATC

33